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Modelling the effects of genetic line and feeding system on methane emissions from dairy systems

Matthew Bell

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Declaration

I certify that the work described in this thesis is my own, except where otherwise stated, and has not been submitted for any other degree or award.

Matthew Bell

Abstract

Dairy cattle make a significant contribution to global methane emissions. Milking cows in the UK make up about a fifth of the total cattle population, with Holstein-Friesian cows being the most common breed. Investigating ways to minimise methane, a potent greenhouse gas (GHG) produced by dairy cows from enteric fermentation and manure, has gained importance in recent years due its role in climate change. Currently, GHG emissions from UK dairy farming are predicted using the Intergovernmental Panel on Climate Change (IPCC) Tier II methodology. The IPCC Tier II methodology and statistical prediction equations from the literature were evaluated for their ability to reliably model methane output using data from the Langhill Holstein-Friesian experimental herd. The Langhill dairy herd is on a long-term breeding and feeding systems experiment, and cows are on average 88% North American Holstein genes. The production systems within the herd represent a range of dairy systems that may be found commercially. Therefore, production values were assumed to be representative of those that could be found in the commercial Holstein-Friesian population, so factors affecting system methane emissions and appropriate mitigation options could be investigated. Prediction equations using dry matter (DM) intake and gross energy intake as input values were the most appropriate equations for reliably estimating daily enteric methane output. However, if DM intake values are not available, the IPCC Tier II method was found to provide a suitable prediction of methane emissions over a cow's lactation and lifetime. This study found that GHG emissions from enteric fermentation and manure, expressed as carbon dioxide equivalents (CO_2-eq.), account for about 66% of dairy system CO_2-eq. emissions, with enteric methane output being the main contributor (34% of system CO_2-eq. emissions). Breeding for increased kilograms of milk fat plus protein production was shown to help reduce dairy system methane emissions. Cows of predominantly North American Holstein genes in this study produced more milk when fed a diet with a low proportion of forage and had lower GHG emissions and land requirement per kilogram energy corrected milk than similar cows fed a diet with a higher proportion of forage. Strategies to mitigate GHG emissions (including methane)

and the environmental impact of dairy systems should seek to select animals that better utilise their feed intake to meet their genetic potential for milk production.

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Contents

Chapter 1 Introduction

1.1 The role of methane in global warming and climate change

In 2007, the Intergovernmental Panel on Climate Change (IPCC) reported that since the year 1750 global atmospheric concentrations of greenhouse gases (GHGs) have increased, most notably in the form of: carbon dioxide from about 280 to almost 379 ppm, methane from 715 to 1774 ppb and nitrous oxide from about 270 to about 319 ppb. The buildup of methane in the atmosphere results from emissions exceeding the potential of the gas to be oxidised by hydroxyl free radicals (formed by the bombardment of ultraviolet radiation on ozone), which would naturally convert methane into carbon dioxide and water vapour (Slanina and Warneck, 1994; Collins *et al.*, 2002). Human activities are believed to be a major source of atmospheric methane. It is estimated that 67% of total atmospheric methane emissions has come from human rather than natural sources, with 19% of total atmospheric methane emissions coming from livestock (17% from enteric fermentation and 2% from manure) (Johnson and Johnson, 1995). As a result of concerns that GHGs produced by human activities are causing permanent changes to the earth's environment, minimising emissions from human activities such as livestock production for food has become increasingly important.

The IPCC concluded that human activities have altered the earth's average near-surface air temperature, partially as a result of GHGs being emitted causing changes in the earth's climate (IPCC, 2007). Due to the variability in lifespan of gases in the atmosphere and the ability of gases to reflect and trap radiant energy, the average potential of a GHG to warm the earth's near-surface air is expressed in carbon dioxide equivalents (CO_2-eq.) emissions (its global warming potential). Methane and nitrous oxide are capable of trapping 21 and 310 times more radiant energy respectively, over a 100 year time horizon, than one kilogram of carbon dioxide (IPCC, 2007).

1.2 Agricultural emissions

Under the Kyoto Protocol agreement in 1997, the UK is required to give annual estimates of CO_2-eq. emissions of GHGs (including methane) from different sources and sinks using the IPCC Tier I, II or III methodologies (IPCC 2006). The IPCC Tier I method uses standard emission factors estimated from *in vivo* experiments, whereas the Tier II and III methods allow country-specific production values to be used to predict emissions (IPCC, 1997; IPCC 2006). Using a combination of Tier I and Tier II methods, the agricultural industry in the UK is estimated to produce 44 of 630 million tonnes of the UK's CO_2-eq. emissions (7% of total UK emissions, and second in importance to the energy industry, which is estimated to produce 85% of total UK emissions) (UKGGI, 2008). The CO_2-eq. emissions from the energy industry come from the production and use of solid, liquid and gas fuel, which include those from agricultural fuel use.

The main GHGs produced by agricultural practices are nitrous oxide, methane and carbon dioxide. In national GHG emission inventories, nitrous oxide and methane are the only GHGs attributed to the agricultural industry (IPCC, 1997; IPCC 2006), which within the UK, are estimated to contribute 58% and 42% of total agricultural emissions respectively (UKGGI, 2008). National inventory emissions discussed here include emissions from enteric fermentation, manure and agricultural soils and crop residues. Emissions do not include those associated with land use change and forestry activities, such as those attributed to deforestation or reforestation for agricultural production. Allocating emissions associated with changing land usage is important when comparing different agricultural commodities. UK agriculture is a major source of methane, producing 37% of total CO_2-eq. emissions, with other notable sources of methane being from landfill, leakage from the gas distribution system and coal mining. Within the agricultural industry, the main sources of methane are from enteric fermentation (84% of CO_2-eq. emissions) and manure (UKGGI, 2008). Manure also produces nitrous oxide emissions. Steinfeld *et al.* (2006) used IPCC methodology to specifically model emissions from livestock activities. The study by Steinfeld *et al.* (2006), which

modelled nitrous oxide, methane and carbon dioxide emissions from livestock activities, found nitrous oxide and methane contributed 6.7% towards the 14% of global CO_2-eq. emissions produced (the remaining emissions being carbon dioxide).

When carbon dioxide emitted from livestock systems are included in a whole systems analysis, sources are mainly associated with fertiliser production, processing activities, electricity and fossil fuel use from the manufacturing and transport of agricultural inputs and products. Respired emissions are not recognised in whole system models for livestock as a net source of carbon dioxide, and it is currently accepted that respired carbon dioxide contribution equates to the net photosynthesis of the consumed plant matter (Steinfeld *et al.,* 2006). Currently this is an accepted assumption within whole system livestock models, which needs further research to quantify its validity. Livestock systems are also a notable source of ammonia. Although ammonia is not a GHG, it can be oxidised to form nitrous oxide. Livestock are estimated to produce 90% of the UK's ammonia emissions from manure (Garnett, 2007).

1.2.1 UK dairy sector emissions

In 2009, there were approximately 1.9 million adult dairy cows in the UK, predominantly of the Holstein-Friesian breed, with an additional 0.5 million replacement animals (Defra, 2009). The dairy sector's total CO_2-eq. emissions are estimated to be 4% of total global GHG emissions (FAO, 2010) and 2% of total UK emissions (Williams *et al.,* 2006); of this, methane is the main GHG produced from dairy systems in developed countries with 52% of emissions (FAO, 2010) from enteric fermentation and manure.

Due to the demand for food, which is projected to grow in the future, the food sector within the UK is reported to account for 22% of total CO_2-eq. emissions (31% in Europe) with half of this coming from meat and dairy products (Garnett, 2007). The dairy sector has an environmental impact through its GHG emissions and resource inputs, which need to be minimised per unit product for sustainable production. The

environmental impact of milk production compares favourably to other livestock products from life cycle assessment (LCA) studies. The LCA method for evaluating the environmental impact of a product is discussed further in Section 1.2.3.3. Williams *et al.* (2006), using the LCA method, found that potentially 95% of a food product's CO_2-eq. emissions can come from on-farm production rather than transport or processing after the product has left the farm. Williams *et al.* (2006) found that the production of milk in the UK is more efficient in terms of its CO_2-eq. emissions per unit product (1.1 tonnes CO_2-eq. emissions/tonne milk) than livestock meat products such as chicken, pork, beef and lamb (4.6, 6.4, 16 and 17 tonnes CO_2-eq. emissions/tonne carcass weight respectively). However, the study by Williams *et al.* (2006) fails to take into account the higher proportion of water in milk and eggs compared to meat (de Vries and de Boer, 2010). Therefore, for comparison of the commodities mentioned above as a source of protein, it would be more appropriate to use 'per unit protein' as the functional unit rather than 'per unit product'. A study by de Vries and de Boer (2010) showed that the production of 1 kilogram of milk protein produces less CO_2-eq. emissions than the production of 1 kilogram of beef protein, and uses less land and energy than 1 kilogram of beef, pork or poultry protein. The functional unit used depends on the objectives of the study, which are discussed further in Section 1.2.3.3.

1.2.2 Enteric and manure methane production

Methane is produced by microorganisms called methanogens as a by-product of anaerobic fermentation. In ruminants such as dairy cattle this occurs predominantly in the rumen rather than the hindgut. Methane is also produced from manure. The processes of methane production as discussed by McDonald *et al.* (1995) and Moss *et al.* (2000) are:

1. Glucose equivalents from plant polymers or starch (cellulose, hemicellulose, pectin, starch, sucrose, fructans and pentosans) are broken down by hydrolysis by extracellular microbial enzymes to form pyruvate in the presence of protozoa and fungi in the digestive tract.

$$\text{Glucose} \rightarrow 2 \text{ pyruvate} + 4H$$

2. The fermentation of Pyruvate involves oxidation reactions under anaerobic conditions producing reduced co-factors such as NADH. Reduced co-factors such as NADH are then re-oxidised to NAD to complete the synthesis of volatile fatty acids (VFAs); the main products being acetate, butyrate and propionate (anions of acetic, butyric and propionic VFAs). The VFAs are then available to be absorbed through the digestive mucosa into the animal's blood stream. Acetate and butyrate production provides a source of hydrogen or alternatively propionate can utilise any available hydrogen, for example:

$$\text{Pyruvate} + H_2O \rightarrow \text{acetate (C2)} + CO_2 + 2H$$
$$2C2 + 4H \rightarrow \text{butyrate (C4)} + 2H_2O$$
$$\text{Pyruvate} + 4H \rightarrow \text{propionate (C3)} + H_2O$$

3. Methanogens eliminate the available hydrogen by using carbon dioxide (CO_2) to produce methane (CH_4):

$$4H_2 + CO_2 \rightarrow CH_4 + 2H_2O$$

Reductions in enteric methane production from ruminants can result from a reduction in rumen fermentation rate or a shift in VFA production (Tamminga *et al.*, 2007). An inverse relationship exists between the production of methane in the rumen and the presence of propionate. If the ratio of acetate to propionate were to be greater than 0.5, then hydrogen will become available to form methane (Johnson and Johnson, 1995). Available hydrogen can accumulate if methanogens fail to use it. This abnormal condition results in dehydrogenation reactions that bring about the re-oxidation of NADH to produce ethanol or lactate, which in turn inhibits microbial growth, forage digestion, and any further production of VFAs (Joblin, 1999; Moss *et al.*, 2000). Dietary

effects on methane production are discussed more fully in Section 1.2.4 on mitigation options.

Typically, rumen gas consists of 40% carbon dioxide, 30 to 40% methane, 5% hydrogen and variable amounts of oxygen and nitrogen from ingested air (McDonald *et al.*, 1995). In ruminants, some 87 to 93% of methane production occurs in the foregut, with the highest rate of production being after eating (Kebreab *et al.*, 2006a). Murray *et al.* (1976) found in sheep that almost 90% of the methane produced in the hindgut was absorbed and expired through the lungs, with the remainder being excreted through the rectum. Johnson *et al.* (1994a) and Grainger *et al.* (2007) estimated rectum enteric methane losses at 7% and 8% of methane output respectively from dairy cows compared to the 1% found using sheep by Murray *et al.* (1976). It is estimated that between 2 to 12% of the gross energy (GE) intake of a dairy cow (typically 6%) is lost as enteric methane, depending on the digestibility of the diet (Smink *et al.*, 2005; Dijkstra *et al.*, 2006). Less digestible dietary components are associated with methane losses as a proportion of GE intake greater than 6%, whereas, dietary components that are easily digested typically lose 2 to 3% of their GE intake as methane (Tamminga *et al.*, 2007).

Manure from livestock can also be a significant source of methane when anaerobic fermentation of organic matter occurs. Liquid manure such as slurry consists of less than 5% solids, with semi solid or solid manure being 5% or more solid content (Kebreab *et al.*, 2006a). Janzen *et al.* (1998) found that slurry increased the potential for methane production due to anaerobic conditions, whereas, less methane is produced by solid manure where more oxygen is present. Methane production from manure is influenced by its organic matter content, as well as climatic factors such as temperature (McAllister *et al.*, 1996; Haeussermann *et al.*, 2006) and agitation from rainfall (Kebreab *et al.*, 2006a). Clemens *et al.* (2006) and Amon *et al.* (2007) studied biogas (a mixture of methane, ammonia and nitrous oxide gases) production, and found that manure in the form of slurry produced more methane with increasing organic matter content. About 16 to 22% of total dairy system methane emissions are emitted from

manure (Hindrichsen *et al.,* 2005). Anaerobic digestion is the most established and efficient technique currently for converting manure methane emissions into a source of energy (Cantrell *et al.*, 2008). There are also other added benefits of using an anaerobic digester, such as reducing unpleasant odour, retaining the loss of nutrients from the system that might otherwise have been lost into the atmosphere and to offset some of the energy used on the farm (Cantrell *et al.,* 2008). An anaerobic digester can potentially capture as much as 68% of total methane produced from manure during warmer summer months, with about half of this same potential during the winter (Clemens *et al.,* 2006).

1.2.3 Techniques to estimate methane emissions

Estimates of methane output from livestock can be costly and difficult to make, especially from large ruminants like cattle. A range of techniques that have been used to estimate methane emissions from ruminant livestock are discussed in reviews by Johnson and Johnson (1995) and Kebreab *et al.* (2006a). Table 1 summarises the main techniques that have been used to estimate methane emissions from enteric or manure sources or both.

Table 1. Methods used to measure methane emissions from ruminant livestock*

Method of measurement	Description
Chamber	Open-circuit indirect respiration calorimeter. Air blown in and extracted out of a chamber. Air concentrations between the incoming and outgoing air are continuously monitored using gas analysers. Chamber conditions are controlled and monitored usually for 48 hours.
Head box, hood or mask	Respired gas volume can be sampled at regular intervals.
ERUCT (Emissions from ruminants using a calibrated tracer)	Typically using the inert sulphur hexafluoride (SF_6) tracer gas. Assumes that the emitted tracer gas from a permeation tube in the rumen simulates the diffusion of any methane emitted. Respired air collected via a capillary tube near the animal's nostrils into a vessel.
Mass balance micrometerological	A known amount of tracer gas released from a known source. Assumes that the emission rate of tracer gas from fixed points simulate the diffusion of methane. Background air samples and a high precision gas analyser are required. Sampling downwind of the source. Captures all emissions.
Room tracer gas	Tracer gas is released into a ventilated room until a steady concentration is reached, after which air samples can be collected. Background air samples are required. Captures all emissions.
Polythene tunnel	Air blown in and extracted out of tunnel. Air concentrations between the incoming and outgoing air are continuously monitored. Captures all emissions.

* All techniques listed are described fully by Kebreab *et al.* (2006a).

An open-circuit indirect respiration calorimeter (chamber) currently provides the most reliable method of obtaining an estimate of individual whole animal enteric methane emissions from eructation and flatulence over a continuous sampling period (Kebreab *et al.,* 2006a). The open-circuit chamber is however costly to construct (Kebreab *et al.,* 2006a) but more suitable for large ruminants like cattle, more so than closed-circuit chambers. There are suggestions that this technique may affect the behaviour of some animals causing depression of appetite (Murray *et al.,* 1999; Sherlock, 2005). The polythene tunnel technique is a more mobile but a similar approach to using a chamber. Due to the polythene tunnel being mobile it is adaptable to different feeding systems such as grazing animals (Lockyer and Jarvis, 1995; Murray *et al.,* 1999). However, Lockyer and Jarvis (1995) and Murray *et al.* (1999) found difficulties in controlling the tunnel's temperature and humidity, and a lower estimate of methane production was recorded compared to chamber measurements.

Less costly techniques, often using the inert sulphur hexafluoride (SF_6) gas as a marker, include the room tracer (Johnson *et al.,* 2002) and mass balance micrometerological methods where the tracer gas is released from fixed points (Kaharabata *et al.,* 2000; Laubach and Kelliher, 2005; Griffith *et al.,* 2008); both require careful monitoring of the sampling environment. Also, the diffusion of the tracer gas should be tested prior to commencing sampling. This can be done by releasing a known amounts of tracer gas and the gas of interest i.e. methane. The temperature, air pressure, humidity and air speed should also be monitored for their consistency in a non-enclosed sampling environment. Controlling the sampling environment would make replicating these techniques consistently on commercial farms difficult. Also, as discussed by Kebreab *et al.* (2006a), use of a tracer gas, such as SF_6, has a long withdrawal period on products from animals exposed to the gas. The ERUCT (emissions from ruminants using a calibrated tracer) technique (Johnson *et al.,* 1994a; Vlaming *et al.,* 2005) or a head box, hood or mask (Belyea *et al.,* 1985; Kelly *et al.,* 1994) solely estimate respired methane emissions from individual animals. This ignores enteric methane from the rectum, which as previously discussed can be as much as 7% or 8% of total enteric methane

production of an animal (Johnson *et al.,* 1994a; Grainger *et al.,* 2007). The ERUCT technique was devised to allow measurement of methane emissions from free ranging and feedlot animals. The studies of Vlaming *et al.* (2005) and McGinn *et al.* (2006) suggest that the ERUCT technique is suitable for estimating respired methane emissions from high forage fed animals and not with diets that result in greater post-ruminal digestion. Even though the ERUCT technique is more open to errors in estimates compared to using a chamber, Grainger *et al.* (2007) suggested these errors can be reduced by removal of outlying estimates and replicating sampling over several days.

More invasive methods of estimating methane production from rumen fluid involve injecting radioactively labelled methane (isotope dilution technique) (Murray *et al.,* 1976; France *et al.,* 1993) or ethane (Moate *et al.,* 1997) into the rumen fluid. Standard methods of analysing air samples for their methane concentration are infrared spectroscopy, gas chromatography, mass spectroscopy or a tuneable laser diode.

1.2.3.1 Measurements

Measurements of enteric methane production from studies on dairy cattle using different sampling techniques are shown in Table 2. The references given in Table 2 are the most recent for different experimental datasets. Table 2 shows that methane output measurements range from 13 to 210 kg methane/head/year across studies. Yan *et al.* (2009) found that dairy cows ranging in live weight from 385 to 747 kg produced between 45 and 199 kg methane/hd/yr (14 to 31 g/kg dry matter (DM) intake) of methane, with beef cattle of 364 to 627 kg live weight producing between 40 and 92 kg methane/hd/yr (13 to 35 g/kg DM intake), with the difference attributed to the amount of DM consumed.

Table 2. Experimental measurements of methane output from dairy cattle

Study	Live weight (kg)	Dry matter intake (kg/day)	Methane (kg/hd/yr)	Sampling method*
Kriss (1930)	162 - 655	1 - 15	39	Chamber
Axelsson (1949)	-	9	79	Chamber
Blaxter and Clapperton (1965)	-	-	40	Chamber
Shibata *et al.* (1993)	-	8 - 18	68 - 122	Chamber
Kinsman *et al.* (1995)	602	18	137	Micrometeorological mass balance
Kirchgessner *et al.* (1995)	450 - 700	-	112	Chamber
Wilkerson *et al.* (1995)	426 - 852	4 - 29	24 - 198	Chamber
Ulyatt *et al.* (1997)	402 - 562	13	96	ERUCT
Kaharabata *et al.* (2000)	600	-	142	Micrometeorological mass balance
Bruinenberg *et al.* (2002)	517	13	95	Chamber
Johnson *et al.* (2002)	-	25	102	Room tracer (SF_6)
Hindrichsen *et al.* (2005)	595	14 - 16	138	Chamber
Woodward *et al.* (2006)	-	14	109	ERUCT
Ellis *et al.* (2007)	526	12	84	Chamber / mask / ERUCT / micrometeorological mass balance
Grainger *et al.* (2007)	496	18	120	ERUCT / Chamber
van Knegsel *et al.* (2007)	572	20	137	Chamber
Yan *et al.* (2010)	379 - 733	8 - 25	72 - 210	Chamber
Mills *et al.* (2009)	173 - 826	2 - 29	13 - 197	Chamber

* Described in Table 1.

1.2.3.2 Prediction equations

This study needed to capture the range of variation found in commercial dairy systems, and it soon became clear that making methane measurements was not a feasible option within the time frame of this study. Reviews by Johnson and Johnson (1995), Wilkerson *et al.* (1995), Benchaar *et al.* (1998), Palliser and Woodward (2002), Mills *et al.* (2003), Ellis *et al.* (2007), Kebreab *et al.* (2006b) and Tamminga *et al.* (2007) have studied the use and performance of different methane output prediction equations. The range of statistical prediction equations published in the literature that have been developed to facilitate the estimation of enteric methane output from dairy cattle are shown in Table 3. Over time, methane output prediction equations have been developed on a broader range of input production values.

Prediction methods can be either dynamic or statistical. Dynamic equations estimate methane output using mathematical descriptions of rumen fermentation. Even though dynamic equations appear to show the greatest degree of adaptability across diet types

and intake level (Benchaar *et al.*, 1998; Kebreab *et al.*, 2006b; Thornley and France, 2007), they require detailed and complex dietary input values. Dynamic equations for estimating methane output have been produced by Baldwin *et al.* (1987) (recommended by Benchaar *et al.* (1998), and Palliser and Woodward (2002)), Lescoat and Sauvant (1995), Pitt *et al.* (1996), Kohn and Boston (2000), Giger-Reverdin *et al.* (2003), van Laar and van Straalen (2004), Danfaer *et al*. (2006), Dijkstra *et al.* (2006) (Benchaar *et al.* (1998) recommended an earlier version of this model) and Offner and Sauvant (2006). Statistical equations offer a more practical solution to predicting methane output using production values such as nutrient intake, milk yield and live weight. Of the statistical methane output prediction equations shown in Table 3, the following were recommended in review studies when their predictions were compared against methane measurements: Blaxter and Clapperton (1965) (recommended by Wilkerson *et al.* (1995)), Moe and Tyrrell (1979) (recommended by Wilkerson *et al.* (1995), Johnson and Johnson (1995), Palliser and Woodward (2002) and Mills *et al.* (2003)), Yan *et al.* (2000) (recommended by van Straalen (2005)) and the non-linear equations using DM intake and metabolisable energy (ME) intake by Mills *et al.* (2003) (recommended by Kebreab *et al.* (2006b) and Ellis *et al.* (2007)). A common recommendation from validation studies on statistical prediction equations is that they can only safely be used within the range of data used in their development. Statistical prediction equations in Table 3 with input variables found in the Langhill data were assessed for their suitability for modelling enteric methane output in Chapter 2 of this study. In the absence of methane output measurements, prediction equations were tested to see how they performed in comparison to assessment criteria developed from the literature and using data with a broader range of input values to those used in their development.

Table 3. Statistical prediction equations from the literature that estimate enteric methane output from dietary inputs and production values for dairy cattle

Source		Equation
Kriss (1930)	g/day	= 18 + 22.5 × DMI
Bratzler and Forbes (1940)	g/day	= 4.012 × TC + 17.68
Axelsson (1949)	MJ/day	= -2.07 + 2.63 × DMI - 0.105 × DMI^2
Blaxter and Clapperton (1965)	MJ/day	= [1.3 + 0.112 × D + FL × (2.37 - 0.05 × D)/100] × GEI
Moe and Tyrrell (1979)	MJ/day	= 3.38 + 0.51 × NFC + 1.74 × HC + 2.652 × C
Holter and Young (1992)	% GEI	= 2.898 - 0.0631 × MY + 0.297 × MF - 1.587 × MP + 0.0891 × CP + 0.1010 × [(FADF/DMI) × 100] + 0.l02 × DMI - 0.131 × F + 0.116 × DMD - 0.0737 × CPD
	% GEI	= 2.927 - 0.0405 × MY + 0.335 × MF - 1.225 × MP + 0.248 × CP - 0.448 × [(ADF/DMI) × 100] + 0.502 × [(FADF/DMI) × 100) + 0.0352 × ADFD
	% GEI	= 227.099 - 2.783 × [(ADFD/DMI) × 100] - 6.0176 × ADFD + 3.607 × CPD + 1.751 × NDSD - 1.423 × CD + 1.203 × HD
Kirchgessner *et al.* (1995)	g/day	= 10.0 + 4.9 × MY + 1.5 × $LWGT^{0.75}$
Johnson and Ward (1996)	g/day	= 41 + 30 × DS + 6 × S + 51 × DCW
Yan *et al.* (2000)	MJ/day	= DEI × [0.094 + 0.028 × (FADF/TADF)] - 2.453 × (FL-1)
	MJ/day	= DEI × [0.096 + 0.035 × (FDMI/DMI)] - 2.298 × (FL-1)
Yates *et al.* (2000)	MJ/day	= 1.36 + 1.21 × DMI - 0.825 × CDMI + 12.8 × NDF
Boadi and Wittenburg (2002)	L/day	= 38.92 + 26.44 × DMI
Mills *et al.* (2003)	MJ/day	= 5.93 + 0.92 × DMI
	MJ/day	= 8.25 + 0.07 × MEI
	MJ/day	= 7.30 + 13.13 × N + 2.04 TADF + 0.33 × S
	MJ/day	= 1.06 + 10.27 × FP + 0.87 × DMI
	MJ/day	= 56.27 - (56.27 + 0) × $e^{[-0.028 \times DMI]}$
	MJ/day	= 45.89 - (45.89 + 0) × $e^{[-0.003 \times MEI]}$
	MJ/day	= 45.98 - (45.98 + 0) × $e^{[cx]}$; cx = -0.0011 × (S/TADF) + 0.0045 × MEI
Hindrichsen *et al.* (2005)	g/day	= 17.1 × DMI + 97.4
	g/day	= 84 + 47 × C + 32 × S + 62 × DS
	g/day	= 91 + 50 × C + 40 × HC + 24 × S + 67 × DS
	g/day	= 123 + 84 × C - 30 × HC + 58 × S + 73 × DS - 95 × L
Yan *et al.* (2005)	L/day	= 47.82 × DMI - 0.762 × DMI^2 - 41
Ellis *et al.* (2007)	MJ/day	= 8.56 + 0.14 × FP
	MJ/day	= 3.23 + 0.81 × DMI
Yan *et al.* (2007)	L/day	= 38.2 + 4.89 × FP × DMI - 0.719 × DMI^2 – 20
	L/day	= 0.666 × LWGT + 2.868 × MY + 75
	L/day	= 39.2 × DMI - 0.588 × DMI^2 + 0.370 × LWGT - 1.698 × MY - 134
Mills *et al.* (2009)	MJ/day	= 74.43 - (74.43 + 0) × $e^{[-0.0163 \times DMI]}$
	MJ/day	= 74.43 - (74.43 + 0) × e[cx]; cx = -0.0187 + 0.0059 / [1 + exp 3.1003)]/0.6127 × DMI
	MJ/day	= (7.16 - 0.101 × DMI)/100 × GEI
	MJ/day	= 2.6861 + 0.0779 × DEI

DMI = dry matter intake (kg/day); CDMI = concentrate DMI (kg/day); FDMI = forage DMI (kg/day); TC = total NDF, sugar and starch (100 g/day); D = digestibility of gross energy at maintenance (%); NFC = non-fibre carbohydrate (kg/day); HC = hemicellulose (kg/day); C = cellulose (kg/day); MY = milk yield (kg/day); MF = milk fat composition (%); MP = milk protein composition (%); CP = crude protein (% DMI); F = fat (% DMI); DMD = DM digestibility (%); CPD = CP digestibility (%); ADFD = acid detergent fibre digestibility (%); NDSD = neutral detergent solubles digestibility (%); CD = cellulose digestibility (%); HD = hemicellulose digestibility (%); DS = sugars (kg/day); DCW = digested cell walls (kg/day); L = lignin (kg/day); LWGT = live weight (kg); DEI = digestible energy intake (MJ/day); MEI = metabolisable energy intake (MJ/day); GEI = gross energy intake (MJ/day); FADF = forage ADF (kg/day); TADF = total ADF (kg/day); FL = multiples of MEI over maintenance; NDF = neutral detergent fibre (kg/kg DM); FP = forage proportion (kg/kg DM); N = nitrogen (kg/day); S = starch (kg/day).

In addition to dynamic and statistical prediction equations for methane output, the IPCC (1997 and 2006) has published methodology for estimating enteric and manure methane emissions from livestock, as mentioned in Section 1.2. Depending on the availability of input values the IPCC Tier I, II or III methodologies can be applied to estimate methane emissions, based on an animal's predicted energy requirements to produce emission factors (IPCC 2006). In the IPCC calculations, it is assumed that 6% of GE intake is lost as enteric methane and the capacity of manure to produce methane is 0.24 m^3/kg volatile solids excreted with a methane conversion factor of 0.01 for solid manure (e.g. from grazing animals) and 0.1 for slurry (UKGGI, 2008).

1.2.3.3 Whole system models

Daily methane output predictions can be incorporated into a whole system model to allow genetic improvement, nutrition and management effects to be assessed. The studies by Cederberg and Mattsson (2000), Casey and Holden (2005), Williams *et al.* (2006), Thomassen *et al.* (2008), Basset-Mens *et al.* (2009) and FAO (2010) used LCA to model the CO_2-eq. emissions associated with different dairy systems. The LCA of a product has become an internationally accepted method for assessing its potential environmental impact (Guinée *et al.*, 2002), and to identify the emission-intensive processes within a product's life cycle. The LCA requires significant amounts of information to reliably account for all inputs and outputs associated with a product (functional unit) produced from a system within the defined boundary. The system boundary largely depends on the goal of the study. The system boundary may be the farming unit, or when comparing the supply of commodities it would also include the transport and processing stages of the supply chain. Typically when comparing dairy systems, the system boundary was the production of raw milk on a farm, which ignores the transport and processing after the milk has left the farm. Additionally, the common functional unit would be one kilogram of energy corrected milk (kg ECM). A weakness of whole system models at present is their ability to account for the impact of any land use change when comparing systems (de Vries and de Boer, 2010).

Using LCA, Williams *et al.* (2006) and Thomassen *et al.* (2008) found organic production produced more CO_2-eq. emissions per unit product than a more intensive conventional dairy system. This study will investigate a range of systems using LCA within the same farming unit. Whole system models have also been developed by Lovett *et al.* (2006) and described by Schils *et al.* (2007) to incorporate effects such as climate, soil conditions and other farm enterprises to assess mitigation options for reducing dairy system emissions.

1.2.4 Mitigation options

Obviously, reductions in emissions could be achieved by simply reducing livestock numbers. However, the global demand for dairy products has been growing rapidly since 2000, with meat and milk consumption projected to double by 2050 (FAO, 2010). Therefore, ways to minimise the methane emissions and environmental impact per unit product from a dairy system are required for sustainable milk production (Capper *et al.*, 2009).

A range of mitigation options for dairy systems is discussed in the following sections:

1.2.4.1 Genetic improvement

Increasing the genetic potential of a cow to produce milk increases dairy system total GHG emissions due a higher feed intake (Lovett *et al.,* 2006). However, methane output per unit product can be reduced by selecting animals on increased feed utilisation efficiency (Hegarty *et al.,* 2007; Yan *et al.*, 2010). Table 4 shows the heritabilities of health, fertility and production traits from studies on the Langhill experimental herd (described in Section 1.3.3). Daily DM intake, milk yield (both averaging 0.40 across studies) and live weight (averaging 0.58 across studies) are moderately heritable traits compared to health and fertility (ranging from 0 to 0.15). Therefore production traits such as DM intake, milk yield and live weight have a better potential for permanent and cumulative genetic improvement over time rather than selecting animals on health and

fertility traits. Genetic improvement is also a cost effective mitigation option (Moran *et al.,* 2007).

Due to the between-animal variation in methane emission per unit DM, Eckard *et al.* (2010) reported that selecting animals based on their enteric methane output could potentially reduce methane losses per unit DM by 10 to 20%. The difference in methane output between animals on the same diet is due to variation in their rumen microbial population. Once individual measurements for total animal methane emissions become more affordable to carry out for a large number of animals, selecting animals on methane output will become possible. Some studies have suggested that the direct selection of animals on their methane production is of little importance (Münger and Kreuzer, 2008; Martin *et al.,* 2010) given its relationship with feed intake, which is a more easily measured trait.

Selecting animals for efficient feed use could bring both higher production and reduced resource requirements. Feed utilisation efficiency can be assessed by feed intake required per unit product or by residual feed intake (Jones *et al.,* 2008). Studies by Okine *et al.* (2003), Nkrumah *et al.* (2006) and Hegarty *et al.* (2007) looking at selecting beef cattle based on a lower residual feed intake (difference between actual and expected feed intake) found that growth performance was not compromised and the lower expected feed intake resulted in less methane produced. Low correlations between residual feed intake and other production traits imply that little or no genetic improvement has previously been made in residual intake as a result of selection on production traits (Jones *et al.,* 2008). However, estimates of lower residual feed intake using production values which are usually more readily available are more appropriate for animals bred for meat rather than milk production. Residual feed intake predictions are based on the estimation of body lipid and protein composition, which change during a lactation when a dairy cow mobilises body energy reserves for milk production. Taking direct feed intake measurements can be costly due to the equipment required, therefore an indirect measure of feed efficiency may be a more appropriate option for

dairy animals, but future work is required to investigate measures that might be correlated with intake. Biologically inactive markers released in the rumen (such as *n*-alkanes) have successfully been used to predict feed intake, however, as with other markers released in this way (i.e. such as SF_6 discussed in Section 1.2.3) there are concerns about the consistency of the marker release rate (Lassey, 2007).

Table 4. Heritabilities from studies carried out on lactating cows in the Langhill herd

	Veerkamp and Brotherstone (1997)	Veerkamp *et al.* (1995)	Pryce *et al.* (1999)
Number of records	1157	377	2516
Trait			
Dry matter intake	0.44	0.36	
Milk yield	0.34	0.45	
Live weight	0.44	0.71	
Mastitis			0.04
Ketosis			0.01
Metritis			0.01
Retained placenta			0.02
Milk fever			0.00
Lameness			0.08
Oestrus not observed			0.05
Conception at first service			0.02
Calving interval			0.09
Days to first service			0.15
Days to first heat			0.13
Days open			0.13

Bauman *et al.* (1985) found that selecting dairy cows on increased productive efficiency with regard to maintenance energy requirements, ME use for milk synthesis, and digestion and nutrient absorption, showed less potential compared to nutrient partitioning and feed intake. The authors also found that improvements in productive efficiency of cows, i.e. the ratio of milk yield to resource input, are due to an increased partitioning of energy intake to milk production and a dilution of maintenance requirement. High milk producing cows with higher feed intakes have been shown to have lower methane outputs per kilogram of milk (kg milk) (Chagunda *et al.*, 2009). Benchaar *et al.* (2001) and Kebreab *et al.* (2006b) reported that methane production is positively correlated with DM intake and level of milk production in dairy cattle. As the feed intake of an animal increases, the percentage of dietary GE intake lost as methane

decreases by an average of 1.6% per unit of intake (Johnson and Johnson, 1995). A faster passage rate due to a higher feed intake level as a result of a higher rate of fermentation, both reduce the rumen retention time of substrate and reduce methane production (Johnson and Johnson, 1995; Ulyatt *et al.*, 1997; Tamminga *et al.*, 2007). Dillon (2006a) found that if cows are to meet their genetic potential for milk production, they need to maximise their feed intake (which is higher in larger animals), which can be achieved using a more digestible total mixed ration (conserved forage and blended concentrate mix) rather than pasture. Robertson and Waghorn (2002) compared the larger North American Holstein-Friesians with its high milk producing potential and high feed intake on a total mixed ration to the smaller and less productive New Zealand genotype selected for better milk production from pasture. Robertson and Waghorn (2002) found that the North American genotype produced between 8 to 11% less methane as a percentage of GE intake on both a total mixed ration and pasture-based diet. The authors suggested the reduction in methane lost as a percentage of GE intake may be partly explained by the increased feeding efficiency associated with a larger animal (i.e. North American genotype) with a greater bite weight compared to a smaller animal (i.e. New Zealand genotype). Larger animals are reported to be more efficient feeders, with a larger jaw size and greater feed intake per bite compared to smaller animals (Dillon, 2006a).

In addition to animal breeding, the production of high quality feed in terms of digestibility, crude protein and ME provision. This study focuses on mitigation options associated with the animal and its feeding system. However, the whole farming system should look to plant and animal breeding for improved animal performance.

1.2.4.2 Nutrition

Diet composition can influence rumen fermentation and reduce methane production as a result of more propionate present or less degradation of food consumed. Improving the quality of food fed to a ruminant is an effective way to manipulate the diet (in terms of neutral detergent fibre, crude protein and ME content) to get better animal performance

and reduced methane production (Benchaar *et al.*, 2001; DeRamus *et al.*, 2003; Yan and Mayne, 2007; Yan *et al.*, 2010). Post-ruminal digestion, particularly in the small intestine, is energetically more efficient with lower methane losses than digestion in the rumen, which can be encouraged by more digestible and higher quality food.

The amount and type of dietary carbohydrate fermented affects the fermentation rate and rumen retention time of substrate, in addition to the hydrogen supply due to the ratio of acetate to propionate. Okine *et al.* (1989) found that the passage rate of substrate and rumen fluid dilution rate (influencing the ratio of acetate to propionate) explained 28% and 25% of variation in an animal's methane production. Cellulose ferments more slowly than hemicellulose, but these structural carbohydrates both ferment more slowly than non-structural and more soluble carbohydrates such as starch and sugars (Eckard *et al.*, 2010). The feeding of starch will also result in more propionate (Tamminga *et al.*, 2007). Cereal-based feeds, often fed as a concentrate blend, are rich in digestible carbohydrate such as starch rather than fibre. Concentrate feeds increase the rate of fermentation of a diet and give rise to elevated levels of propionate as a result of a lower rumen pH, which help to reduce methane production (Holter and Young, 1992; Johnson and Johnson, 1995; Lovett *et al.*, 2006; Yan and Mayne, 2007). With regard to forages, increasing the digestibility of forage fed by reducing fibre content can reduce methane production. Feeding maize silage (Yates *et al.*, 2001) or a legume-based silage (Benchaar *et al.*, 2001) rather than grass silage has been found to reduce methane production. Also, silage is generally more digestible than hay (Benchaar *et al.*, 2001) and adding molasses or urea to straw made it more digestible (Huque and Chowdhury, 1997), which in both cases reduced methane production. Forage methane production can be minimised by lower fibre content and high soluble carbohydrate (influenced by maturity), and C3 grasses rather than C4 (Eckard *et al.*, 2010). Moss (1992) and Johnson and Johnson (1995) suggested the grinding or pelleting of forages to increase their surface area and digestibility to help reduce methane production.

It is well recognised that by compensating rumen digestion for post-ruminal digestion in the small intestine and by promoting the production of propionate rather than acetate, methane losses per unit intake can be reduced. The addition of feed additives to a ruminant's diet are being extensively evaluated for their effect on reducing methane emissions. The benefit in animal productivity and reduction in methane production relative to the cost of using different additives is continually being evaluated. Supplementation of diets with additives such as fats has been found to reduce methane production (Holter and Young, 1992; Johnson and Johnson, 1995; Lovett *et al.,* 2003; McGinn *et al.,* 2004; Beauchemin and McGinn, 2006; Jordan *et al.,* 2006) particularly fats with C8 to C16 chain length such as coconut oil (Dohme *et al.,* 2000; Giger-Reverdin, 2003), however the effect, which is a suppression on fermentation, is not lasting (Johnson *et al.,* 2002; Woodward *et al.,* 2006). Suppressing fermentation by supplementing the diet with fat inhibits methanogens and protozoa, and subsequent fibre digestion with a shift towards more propionate present rather than acetate (Eckard *et al.,* 2010). Likewise, the use of ionophores in feed (particularly monensin and salinomycin) and spices (Chaudhry and Khan, 2010) that modify the rumen microflora (Mohammed *et al,* 2004) can reduce methane losses (Moss *et al.,* 2000; Boadi *et al.,* 2004; Kebreab *et al.,* 2006a; Odongo *et al.,* 2007) and encourage a shift towards propionogenesis. However eventually the rumen microflora show some resistance and the suppression ceases (Johnson *et al.,* 1994b; Sauer *et al.,* 1998; McGuffey *et al.,* 2001). These feed additives are banned within the European Union due to the fears of residues appearing in the milk.

Other feed additives tested include the use of plant compounds such as tannins (inhibiting methanogens) and saponins (inhibiting protozoa), which reduce the digestibility of dietary fibre (Animut *et al.,* 2007), and organic acids such as fumarate, malate and acrylate which act as an alternative hydrogen acceptor (McAllister and Newbold, 2008), but results for effects on methane production and animal performance are variable (Martin *et al.,* 2010). Probiotics (acetogens and yeast) have been found to reduce methane output (Boadi *et al.,* 2004) but not by others (Martin *et al.,* 2010).

Overall, unless yeast by-products can reliably be used to reduce methane production, the most cost-effective additive for reducing production appears to be the addition of cellulase and hemicellulase enzymes to a ruminant's diet, which not only improved fibre digestion but also productivity (Beauchemin *et al.,* 2008).

1.2.4.3 Management

Systems methane emissions can be minimised by improvements in herd health and fertility (improving longevity and productivity), and by reducing the number of replacement animals retained on the farm (Garnsworthy, 2004; O'Mara, 2004; Tamminga *et al.*, 2007). Garnsworthy (2004) suggested that improving herd fertility in the UK to 1995 levels could amount to a 24% reduction in methane emissions per cow by improved efficiencies of reduced herd replacements and calving interval length.

As discussed in Section 1.2.4.2, the quality of food given to ruminants can influence their emissions. Management to enhance the quality of feed given to animals, particularly from pasture (which can vary in quantity, composition and maturity), can influence nutrient intake and reduce the milk production potential of the animal (Kennedy *et al.*, 2003). To minimise emissions in a housed environment, manure should be frequently removed to an air-tight storage area (with reported reductions in GHG emissions of 10 to 13% by Clemens *et al.,* 2006), with manure applied to fields by injection if possible (Weiske *et al.*, 2006). The longer manure is stored and also if it is agitated, then greater amounts of methane are emitted (Kebreab *et al.,* 2006a). Clemens *et al*. (2006) and Weiske *et al.* (2006) found that anaerobic digesters can be an efficient way to reduce GHG emissions from housed animal manure as mentioned previously. To summarise, improvements to reduce emissions and resource use can be made through better management of animals and nutrition (efficient energy intake utilisation towards milk production as discussed in Section 1.2.4.2), crops and soil (to promote crop quality and production) and storage and application of farm manure (to retain nutrients and harness emissions).

Rumen manipulation and the use of immunisation to suppress methanogenic activity or defaunating the protozoa population in the rumen has been tested and not found to consistently reduce emissions without affecting animal performance (Martin *et al.*, 2010). Biological control methods to inhibit methanogenesis by adding bacteriocins and acetogens have also been tested, but with no lasting effect on reducing methane production (Eckard *et al.*, 2010; Martin *et al.*, 2010). Martin *et al.* (2010) suggest that the sequencing of the genome of *Methanobrevibacter ruminantium* by New Zealand scientists will help identify immunological targets for future vaccine development. The use of a product such as Bovine Somatotrophin (BST), which is a hormone that stimulates milk production, has been found to help reduce methane emissions per unit product (Johnson *et al.*, 1997); however, the use of this hormone is banned in the European Union due to the fears of residues appearing in the milk.

1.3 The thesis

1.3.1 Rationale

The scope for reducing agricultural GHG emissions has gained importance in recent years to help meet future targets for GHG reductions. Future targets for the UK under the Kyoto Protocol are to reduce direct emissions to 12.5% below 1990 figures over the period of 2008 to 2012 (UNFCCC, 1997). Yet the UK government has set further targets of reducing its total GHG emissions by 80% by 2050 (as set out in the UK's Climate Change Programme, 2006), with the Scottish government also setting a target of 80% reduction by 2050 with 42% being by 2020 (Climate Change (Scotland) Act, 2009). Generally, government plans for agriculture are to promote efficient use of resources per unit product to help meet these targets.

In 1991, van Gardingen had already highlighted three main needs to assess the GHG emissions from agriculture, which were: better estimates of emissions, technology to reduce emissions and policies to help limit emissions. Moss (1992) added to this the

need to study diet and microbial manipulation, and models to determine emissions. These questions are still being answered today.

1.3.2 Objectives

This thesis used extensive and detailed data from the Langhill dairy herd in Scotland, which is on a long-term breeding and feeding systems experiment. The data were used to model production values that could be considered representative of those found in commercial Holstein-Friesian dairy systems, from which strategies to mitigate methane emissions could be assessed. The objectives of this thesis were to:

1. Assess how reliable and suitable existing methane output prediction equations are for production values that may be found in commercial Holstein-Friesian dairy systems;
2. Assess the effect of breeding for milk yield, diet and management on reducing enteric methane emissions;
3. Assess the effects of genetic line and feeding system on total methane emissions from dairy systems;
4. Assess the effect of improving cow productivity, fertility and longevity on the global warming potential of dairy systems;
5. Suggest adaptations and strategies to mitigate emissions from dairy systems.

The findings of this study form the structure of the thesis, which are presented in Chapters 2 to 6. The results shown in Chapter 2 are an updated version of those published by Bell *et al.* (2009) in Aspects of Applied Biology, with additional methane output prediction equations by Mills *et al.* (2009) having been added to the study. Chapter 3 is published in Animal Production Science (Bell *et al.*, 2010a). Chapter 4 is published in Animal Feed Science and Technology (Bell *et al.*, 2011). Supplementary material to Chapter 5 is shown in Appendix A and published in The Veterinary Record (Bell *et al.*, 2010b).

1.3.3 Data

The data from the Langhill experimental herd were collected by farm staff from 1990 to 2009 and stored in a database, from where the information for this thesis was obtained. To ensure comparability with commercial units the dataset consists of information from all the cows in the experiment irrespective of their state of health. The experiment is one of the longest running genetic line × feeding system projects in the world and its structure is briefly described below:

1. The herd consists of genetic lines selected for kilograms of milk fat plus protein (Select line) or selected to remain close to the average genetic merit for milk fat plus protein production for all animals evaluated in the UK each year (Control line).
2. Cows in each genetic line × feeding system (2 × 2 experiment) were controlled so that approximately equal numbers of Select and Control cows were offered each diet. In addition to this, cows were kept in the herd for at least three lactations unless a cow was required to be culled from the milking herd due to poor health or fertility. Culling was recorded when a cow's productive life ceased. After three lactations cows were replaced on the experiment if a suitable heifer replacement was available. On average, both Select and Control genetic lines were 88% North American Holstein genes.
3. From 1990 to 2002 the herd was managed at The University of Edinburgh's Langhill farm, near Edinburgh (Farm 1). In June 2002 the herd moved to the SAC Dairy Research Centre, in Dumfries (Farm 2). The experiment at Langhill Farm was described by Veerkamp *et al*. (1994) and at the SAC Dairy Research Centre by Pollott and Coffey (2008). Whilst at The University of Edinburgh, the milking herd was divided into two feeding systems with diets formulated to achieve, over a full lactation, proportions in the total DM of concentrate, brewers grains and silage of 0.20:0.05:0.75 (referred to as the High Forage diet fed at Farm 1) and 0.45:0.05:0.50 (referred to as the Low Forage diet fed at Farm 1). Cows on the High Forage and Low Forage diets at Farm 1 had annual average

intakes of concentrate of approximately 1,500 and 2,500 kg respectively, with summer grazing. From 2002 the herd was managed on two contrasting management systems. Half of the herd was kept indoors on a non-grazing system and fed a low forage diet formulated to achieve a target ME content of 12.3 MJ/kg DM and crude protein content of 185 g/kg DM (referred to as the Low Forage diet at Farm 2). Over a full lactation, Low Forage diets at Farm 2 were about 50% forage in the total DM. Forage was fed as grass silage, maize silage or ammonia treated wheat silage in a total mixed ration at Farm 2. The other half of the herd received a high forage diet with summer grazing, when sufficient pasture was available (referred to as the High Forage diet at Farm 2). The High Forage diet at Farm 2 was formulated to achieve a target ME content of 11.5 MJ/kg DM and crude protein content of 180 g/kg DM. Over a full lactation, the High Forage diet at Farm 2 was about 75% forage in the total DM. Cows on a Low and High Forage diet at Farm 2 had annual average intakes of concentrate of approximately 1,200 and 3,000 kg respectively.

4. Feed analysis was carried out at the SAC Analytical Lab, Edinburgh. Dietary ME was estimated using the prediction equation developed by Thomas *et al.* (1988).
5. Whilst indoors, cows were fed *ad libitum* as a total mixed ration (conserved forage and blended concentrate mix) and feed intakes were recorded before 2001 using Calan Broadbent gates (American Calan, Inc., Northwood, NH, USA) or after 2001 using HOKO automatic feed measurement gates (Insentec BV, Marknesse, The Netherlands).
6. Data was obtained for lactating and non-lactating animals (herd replacements, lactating and dry cows):
    a. Lactating cow data –
        i. Daily feed intakes were measured on 3 days out of 6 whilst indoors. Feed intakes included concentrate fed whilst in the milking parlour.
        ii. Live weights were measured weekly before June 2002 after the morning milking and three times a day after each milking from

June 2002 onwards. Body condition score was recorded weekly by a single trained operator before 2002 and by three trained operators after 2002, using a 0 to 5 scale with 0.25 intervals, where 0 is very thin and 5 is very fat (Lowman *et al*., 1976). Live weight and condition score were measured within 48 hours of calving and when cows were dried off. Daily milk yields were the sum of two and three milkings per day for Farms 1 and 2 respectively. The fat and protein compositions of the milk were recorded weekly as averages over the two or three daily milkings.

b. Dry cow data:

i. Different diets were fed to dry cows at Farm 1 and 2, and feed intakes were measured daily when cows were indoors. During the period of July 2001 to October 2001, cows at Farm 1 were fed a pre-dry period diet (D1) followed by a second diet (D2). The ME and crude protein contents of the D1 and D2 diets were: 11.5 and 8.5 MJ/kg DM and 182 and 77 g/kg DM respectively. From September 2004 to January 2006, cows at Farm 2 were fed an early drying off diet (D3) and then either a high forage (D4) or a low forage transition diet (**D5**) as they got closer to calving, depending on their milking diet. On average the ME and crude protein contents of the D3, D4 and D5 diets were: 7.3 ± 0.5, 5.9 ± 0.5 and 6.1 ± 0.2 MJ/kg DM and 107 ± 6, 72 ± 14 and 99 ± 12 g/kg DM respectively.

ii. From June 2004 at Farm 2, dry cows were weighed weekly.

7. The chemical composition of pasture was assumed to be constant based on 17 weekly samples for analysis, taken only during the summer grazing period of 2006. The average chemical composition of the pasture was: 195 ± 38, 627 ± 18, 225 ± 31, 43 ± 17 g/kg for DM, neutral detergent fibre (NDF), crude protein, sugar and 10.5 ± 0.2 MJ/kg for ME respectively (mean ± s.d.). There was no significant trend in the ME content of the pasture across the 2006 grazing period.

8. Health and fertility problems during each lactation were recorded for each cow. The main health and fertility problems found in the Langhill herd were:
    a. Abortion;
    b. Abnormal oestrus cycle (anoestrus, not seen in heat, a repeat cycle, sub oestrus but not including cows with a cystic ovary);
    c. Claw horn lesions including ulcers, haemorrhaging, white line disease and abscesses of the claw,
    d. Cystic ovary (at either ovary);
    e. Diseases of the digital skin (infection of the skin surrounding the claw, including foul of the foot and growths);
    f. Displaced abomasum;
    g. Ketosis;
    h. Mastitis (in at least one quarter);
    i. Retained placenta;
    j. Twinning;
    k. Uterine infection.

Chapter 2 Modelling dairy system production values to predict methane output[1]

2.1 Summary

The aim of this study was to develop a robust way of estimating the methane output of dairy cattle over a broad range of production values. Statistical prediction equations derived from the literature were assessed for whether they provided sensible methane output predictions. Data from the Langhill Holstein-Friesian dairy herd were obtained from November 1990 to October 2007 for lactating cows whilst indoors. Prediction equations were assessed in the absence of methane measurements, using criteria based on available published information and comparisons within the dataset. The results from this study confirm that most published methane prediction equations can only safely be used within the range of data used in their development. However, a non-linear equation based on dry matter (DM) intake and another using gross energy (GE) intake and DM intake as input variables were identified as the most reliable prediction equations for the broad range of input values seen in the Langhill data, and thus for the range of systems found commercially.

Key Words: Dairy cow, methane output, predictions, reliability.

2.2 Introduction

Interest in measuring methane has moved from a focus on nutritional inefficiency (Blaxter and Clapperton 1965) to one of contributing to climate change (Johnson and Johnson 1995; IPCC 2007). About 52% of the 4% of global greenhouse gas emissions contributed by the dairy sector is in the form of methane (FAO 2010).

[1] Previous version published by Bell *et al.* (2009) in Aspects of Applied Biology.

Different techniques have been used to predict methane output. The main technique for predicting emissions is by using feed composition characteristics, but other techniques such as *in vitro* incubation and molar distribution of VFA have been tried to determine emissions from different feeds (Johnson and Johnson 1995; Sherlock 2005; Tamminga *et al.* 2007). Several studies have compared the usefulness of different prediction equations for methane output from dairy cows, such as Johnson and Johnson (1995), Wilkerson *et al.* (1995), Benchaar *et al.* (1998), Palliser and Woodward (2002), Mills *et al.* (2003), Kebreab *et al.* (2006b) and Tamminga *et al.* (2007). There are two main types of equation to help predict enteric methane production: dynamic or statistical equations. Dynamic equations estimate methane output using mathematical descriptions of rumen fermentation and detailed dietary information. Dynamic equations appear to show the greatest degree of adaptability across diet types and intake level (Benchaar *et al.* 1998; Kebreab *et al.* 2006b; Thornley and France 2007). In comparison, statistical prediction equations use production values such as nutrient intake (of dietary components, energy and DM), milk yield and live weight, which in a practical sense are easier to obtain. However, it is well recognised that the success or suitability of a statistical prediction equation is dependent on the reliability of input variables, the range of values that the equation was developed from and the equation's ability to take account of the non-linear relationship between feed intake and methane output (Mills *et al.* 2003; Kebreab *et al.* 2006b), as the proportion of GE lost as methane declines as DM intake increases.

The objectives of this study were: 1) to identify a range of statistical prediction equations for methane output from the literature that could be applied to a range of data values that may be found in commercial dairy farming systems and 2) to test whether these equations could be used outside the range of values on which they were developed.

2.3 Materials and Methods

2.3.1 Data

The study period was from November 1990 to October 2007 for lactating cows whilst indoors. The data are described in Section 1.3.3. The average weekly milk yield, DM intake and live weight ranged respectively from 0.2 to 65.7 kg milk/day (99% reference range of 5.8 to 49.6 kg/day), 1.4 to 35.4 kg DM intake/day (99% reference range of 10.3 to 28.3 kg/day) and 388 to 919 kg live weight (99% reference range of 443 to 830 kg) (Table 5), which represent broad ranges for dairy cows compared to other experimental studies (Table 6).

Table 5. Average weekly production and dietary intake values for cow in this study

		Mean (s.d)	Range
Milk yield	kg/day	27.7 (8.5)	0.2 - 65.7
Dry matter intake	kg/day	19.3 (3.5)	1.4 - 35.4
Live weight	kg	636 (75)	388 - 919
Gross energy intake	MJ/day	371 (71)	13 - 684
Digestible energy intake	MJ/day	260 (51)	10 - 490
Metabolisable energy intake	MJ/day	226 (44)	15 - 449
Acid detergent fibre (ADF)	kg/day	4.8 (0.8)	0.4 - 9.2
Starch	kg/day	2.6 (1.0)	0.3 - 6.2
Carbohydrate	kg/day	10.3 (1.8)	0.8 - 17.9
Crude protein	kg/day	3.5 (0.7)	0.2 - 6.6
Forage ADF	g/day	256 (41)	140 - 361
Forage in total dry matter	%	79.3 (9.6)	53.9 - 100
Total mixed ration in diet	%	95.4 (1.8)	33.9 - 100

The data included cows that were ill or were otherwise feeding poorly, hence the low DM intakes. The average nutrient intake of cows is shown in Table 5. Food components and the mixed ration were analysed at the SAC Analytical Lab, Edinburgh, except for GE (Rowett Research Institute, 1976; Wainman *et al.*, 1979; Wainman *et al.*, 1981; Wainman *et al.*, 1984; Wainman and Dewy, 1989) and digestible energy (DE) (MAFF, 1990).

2.3.2 Predicting methane output

Methane output was predicted using a range of equations from the literature, shown in Table 6, using input values taken from lactating cows in the Langhill herd. It should be

noted that individual cow methane measurements were not available for the Langhill cows, therefore a selection criteria based on information from the literature was developed. The selection criteria was used to identify a suitable predictor of methane output for the dataset in this study. Statistical prediction equations were chosen from those identified in Table 3 (in Section 1.2.3.2) based on availability of input variables. Table 6 also includes a description of the data on which the prediction equation was developed, with number of experimental observations (N), mean or range of daily milk yields, daily DM intakes, live weights, daily methane outputs and the correlation or R-squared value for the equation (or from other validation studies).

There were a possible 25 prediction equations (x[1] to x[25]) for daily methane output that could be used. The equations used in this study were from: Kriss (1930), x[1]; Bratzler and Forbes (1940), x[2]; Axelsson (1949), x[3]; Blaxter and Clapperton (1965), x[4]; Kirchgessner *et al.* (1995), x[5]; Yan *et al.* (2000), x[6] and x[7]; Yates *et al.* (2000), x[8]; Mills *et al.* (2003), x[9] to x[15]; Hindrichsen *et al.* (2005), x[16]; Yan *et al.* (2005), x[17]; Ellis *et al.* (2007), x[19]; Yan and Mayne (2007), x[19] to x[21]; Mills *et al.* (2009), x[22] to x[25]. All equations from the literature were developed using data from dairy cows and methane calorimeter measurements, with Blaxter and Clapperton (1965), Bratzler and Forbes (1940), Ellis *et al.* (2007), Kriss (1930) and Yan *et al.* (2000) also including beef animals and Ellis *et al.* (2007) included data from SF_6 and micrometeorological methane measurements.

Table 6. Prediction equations for methane output (CH_4 MJ/day) that could be used on the Langhill herd dataset from those identified in Table 3 of Section 1.2.3.2, as well as a description of the data on which they were developed

Equation	N	Milk Yield (kg/day)	Dry matter intake (kg/day)	Live weight (kg)	Methane (MJ/day)	R-squared or correlation coefficient (c) (for original data unless stated)
Kriss (1930)	= (18 + 22.5 × DMI) × 0.05565	24	-	1-15	162-655	6	0.94 (c); 0.65[†].
Bratzler & Forbes (1940)	= (17.68 + 0.0401 × TC) × 0.05565	130	-	-	-	-	0.94 (c).
Axelsson (1949)	= -2.067 + 2.636 × DMI - 0.105 × DMI^2	176	-	9	-	12	0.58; 0.24[†].
Blaxter & Clapperton (1965)	= [1.3 + 0.112 × D + FL × (2.37 - 0.05 × D)/100] × GEI	615	-	-	-	-	0.51[†].
Kirchgessner *et al.* (1995)	= 10.0 + 4.9 × MY + (1.5 × $LWGT^{0.75}$) × 0.05565	153	10-30	-	450-700	17	0.60
Yan *et al.* (2000)	= DEI × [0.094 + 0.028 × (FADF/TADF)] - 2.453 × (FL-1)	322	3-49	6-24	416-733	4-30	0.89
Yan *et al.* (2000)	= DEI × [0.096 + 0.035 × (FDMI/DMI)] - 2.298 × (FL-1)	322	3-49	6-24	416-733	4-30	0.89
Yates *et al.* (2000)	= 1.36 + 1.21 × DMI - 0.825 × CDMI + 12.8 × NDF	140	-	14-28	628	15-29	0.54
Mills *et al.* (2003)	= 5.93 + 0.92 × DMI	159	14.2-59.7	13-28	494-826	16-30	0.74, 0.85, 0.67[§]; 0.65[†]; 0.45[‡].
Mills *et al.* (2003)	= 8.25 + 0.07 × MEI	159	14.2-59.7	13-28	494-826	16-30	0.63, 0.83, 0.78[§]; 0.53[†].
Mills *et al.* (2003)	= 7.3 + 13.13 × N + 2.04 × TADF+ 0.33 × S	159	14.2-59.7	13-28	494-826	16-30	0.74, 0.62, 0.46[§].
Mills *et al.* (2003)	= 1.06 + 10.27 × FP + 0.87 × DMI	159	14.2-59.7	13-28	494-826	16-30	0.77, 0.30, 0.25[§]; 0.54[†].
Mills *et al.* (2003)	= 56.27 - (56.27 + 0) × $e^{[-0.028 \times DMI]}$	159	14.2-59.7	13-28	494-826	16-30	0.79, 0.87, 0.68[§]; 0.66[†].
Mills *et al.* (2003)	= 45.98 - (45.98 + 0) × $e^{[-0.003 \times MEI]}$	159	14.2-59.7	13-28	494-826	16-30	0.75, 0.88, 0.78[§]; 0.56[†].
Mills *et al.* (2003)	= 45.98 - (45.98 + 0) × $e^{[cx]}$; cx = -0.0011 × (S/TADF) + 0.0045 × MEI	159	14.2-59.7	13-28	494-826	16-30	0.70, 0.88, 0.83[§]; 0.57[‡].
Hindrichsen *et al.* (2005)	= (17.1 × DMI + 97.4) × 0.05565	35	21	14-16	595	21	0.71
Yan *et al.* (2005)	= (47.82 × DMI - 0.762 × DMI^2 - 41) × 0.03954	315	3-49	5-25	385-747	7-30	0.75
Ellis *et al.* (2007)	= 3.272 + 0.736 × DMI	172	-	3-20	206-740	2.8-25	0.68
Yan & Mayne (2007)	= [(38.2 + 4.89 × FP1) × DMI - 0.719 × DMI^2 - 20] × 0.03954	386	3-49	5-25	385-747	7-30	0.68
Yan & Mayne (2007)	= (0.666 × LWGT + 2.868 × MY +75) × 0.03954	386	3-49	5-25	385-747	7-30	0.73
Yan & Mayne (2007)	= (39.2 × DMI - 0.588 × DMI^2 + 0.370 × LWGT - 1.698 × MY - 134) × 0.03954	386	3-49	5-25	385-747	7-30	0.61
Mills *et al.* (2009)	= 74.43 - (74.43 + 0) × $e^{[-0.0163 \times DMI]}$	1819	0.6-60	2.1-28.7	173-826	2-30	0.91
Mills *et al.* (2009)	= 74.43 - (74.43 + 0) × $e^{[cx]}$; cx = -0.0187 + 0.0059 / [1 + exp (S/TADF - 3.1003)]/0.6127 x DMI	1819	0.6-60	2.1-28.7	173-826	2-30	0.94
Mills *et al.* (2009)	= (7.16 - 0.101 × DMI)/100 × GEI	1819	0.6-60	2.1-28.7	173-826	2-30	0.56
Mills *et al.* (2009)	= 2.6861 + 0.0779 × DEI	1819	0.6-60	2.1-28.7	173-826	2-30	0.96

DMI = dry matter intake (kg/day); CDMI = concentrate DMI (kg/day); FDMI = forage DMI (kg/day); TC = total NDF, sugar and starch (g/day); D = digestibility of gross energy at maintenance (%); MY = milk yield (kg/day); LWGT = live weight (kg); DEI = digestible energy intake (MJ/day); MEI = metabolisable energy intake (MJ/day); GEI = gross energy intake (MJ/day); FADF = forage acid detergent fibre (kg/day); TADF = total ADF (kg/day); FL = multiples of ME intake over maintenance; NDF = neutral detergent fibre (kg/kg DM); FP = forage proportion (kg/kg DM); N = total dietary nitrogen (kg/day); S = total dietary starch (kg/day); The following assumptions were made: 1 g methane = 0.05565 MJ; 1 litre methane = 0.03954 MJ; N = 16% of CP. [†] from Ellis *et al.* (2007); [‡] from Kebreab *et al.* (2006b); § from Mills *et al.* (2003) for CEDAR, ARINI and American data, and ARINI data only.

Prediction equations from the literature were assessed against a prediction of the possible methane producing capabilities of the feed given to animals, which was calculated using data from *in vivo* experiments at the Rowett Research Institute Feedingstuffs Evaluation Unit (Rowett Research Institute, 1976; Wainman *et al.*, 1979; Wainman *et al.*, 1981; Wainman *et al.*, 1984; Wainman and Dewy, 1989). A prediction of the methane output from feed consumed was calculated based on the average percentage of dietary GE lost as methane from the ingredients used plus two standard deviations (referred to as "dietary methane value" x[26]) from the Feedingstuffs Evaluation Unit data. The dietary methane value for the associated amount of GE intake lost as methane in megajoules per day was then obtained. The main ingredients used in diets and their associated methane output (% GE ± s.d.) were: Alkalage (8.8 ± 1.4%), barley (10.6 ± 1.7%), distillers' dark grains (4.9 ± 1.4%), draff (2.7 ± 2.4%), grass silage (7.7 ± 0.8%), maize gluten feed (8.7 ± 2.1%), maize silage (8.0 ± 0.8%), parlour nuts (9.1 ± 0.7%), rapeseed meal (7.1 ± 11.8%), soya (2.8 ± 4.2%), soyabean meal (10.7 ± 3.5%), straw (6.7 ± 2.2%), sugar beet pulp (11.4 ± 1.9%), wheat (10.3 ± 2.7%) and white fish meal (2.9 ± 6.4%). The proportion of methane output predictions for equations x[1] to x[25] that fell above the dietary methane value were determined to assess the variation in predictions associated with each equation (in the absence of information from the literature showing the variation associated with all equation assessed) and as a means of assessing the confidence in predictions produced. The dietary methane prediction does not take into account the decline in methane output per unit of DM intake with increasing DM intake. Also, any effect on methane output as a result of mixing dietary ingredients in a total mixed ration was not taken into account. Daily predicted methane output was calculated from all animals where input values were available. Methane predictions were only done on days when the DM intake was known when cows were indoors for the whole day, so that comparisons are consistent between prediction equations.

2.3.3 Records and analysis

Daily records were averaged across weeks to help remove outlying values. During the study period there were 61,369 average weekly DM intake records from 960 lactating housed cows (24,717, 17,030 and 19,622 for parities 1, 2, and 3 or 3+ respectively). The data were analysed using Genstat Version 11.1 (Lawes Agricultural Trust, 2006). Methane output predictions were compared across a range of DM intakes due to this being the most common input variable across all equations used and measured daily DM intakes were available. R-squared values, Spearman rank correlation coefficients and Pearson correlation coefficients were used to show the difference between prediction equations. Significance was attributed at $P < 0.05$.

Criteria for assessing the suitability of methane prediction equations for the data from the Langhill herd were whether:

1. Graphically predictions approached the origin at low DM intakes;
2. The methane output predictions followed a non-linear positive profile per unit DM intake;
3. There are no methane output predictions that fell above the dietary methane value;
4. The equation had a good data coverage, whereby methane output predictions are generated from a high proportion of available weekly records across the full range of DM intakes seen in the dataset;
5. The prediction equation generated methane output values with a high and positive rank correlation (assessed at 0.70 or above) to the majority of other equations assessed;
6. It had a high R-squared value or correlation in other validation studies from the literature;
7. The dataset the prediction equation was developed on has a broad range of DM intakes, milk yields and live weight values comparable with the Langhill production values.

To assess the data coverage of prediction equations across the full range of DM intakes, the range of DM intakes seen in the Langhill data from 1.4 to 35.4 kg/day was split into quartiles and the proportion of methane output predictions from each equation were determined for each quartile. In addition to this, the proportion of weekly records producing methane output predictions using each equation was assessed. Even though the accuracy of prediction equations could not be assessed (due to the absence of methane measurements), the important aspects of a reliable equation for future modelling of methane output of animals with a similar range of production values to the Langhill dataset are criteria one to four. If criteria one to four are met by an equation, then the additional criteria (five to seven) will undoubtedly also be met.

2.4 Results

The average proportion of GE intake lost as methane for the dietary methane value prediction x[26] was 10.3 ± 0.4% (ranging from 9.4% to 11.6%). The proportion of GE intake lost as methane reflects the variation in dietary components fed to cows. Ingredients used in the total mixed ration with relatively low average methane outputs as a percentage of GE were soya, and by-products from other industries such as distillers' dark grains, draff and white fish meal. However, soya and white fish meal were associated with large standard deviations, as shown above.

Table 7 shows the proportion of weekly records producing methane output predictions using each equation and their distribution across the range of DM intakes seen in the Langhill data. In terms of data coverage, the prediction equations can be placed in one of three groups based on their percentage coverage of the data; the prediction equations with high data coverage of 70% or more of weekly records are x[1], x[3], x[5], x[8], x[9], x[10], x[13], x[14], x[16], x[17], x[18], x[22], x[24], x[25], x[26], medium coverage of between 29% and 49% are x[2], x[4], x[7], x[12], x[19], x[20], x[21] and low coverage of <8% of weekly records are x[6], x[11], x[15], x[23]. A lack of input values for equations with medium to low data coverage may compromise their

performance in this study. Fig. 1 shows that at lower DM intake levels and within the range of daily DM intakes that the majority of equations were developed on (about 5 to 15 kg/day), several equations give similar methane output predictions. If used outside of the range of daily DM intakes they were developed on, some equations give unrealistic results, such as equations x[3] and x[4] giving negative predictions (Table 7), and along with equations x[15], x[17], and x[19], showing a decline in predicted methane output at high DM intakes (Fig. 1).

Table 7. Percentage of total weekly records producing predictions, distribution of records across the range of dry matter (DM) intakes seen in the dataset from 1.4 to 35.4 kg/day and predicted methane output using different equations

				Methane output (MJ/day)		
Equation		% of records	Distribution of records across DM intake quartiles (%)	Mean (s.d)	Range	% of values falling above dietary methane value
Kriss (1930)	x[1]	100	25, 25, 25, 25	25.1 (4.3)	2.7 - 45.4	0.00
Bratzler & Forbes (1940)	x[2]	31	24, 25, 27, 24	23.9 (4.0)	2.7 - 41.0	0.00
Axelsson (1949)	x[3]	100	25, 25, 25, 25	8.0 (5.5)	-40.9 - 14.4	0.00
Blaxter & Clapperton (1965)	x[4]	42	23, 24, 27, 26	17.8 (2.3)	-0.5 - 44.1	0.01
Kirchgessner *et al.* (1995)	x[5]	70	27, 24, 25, 24	18.1 (2.8)	7.1 - 29.3	0.17
Yan *et al.* (2000)	x[6]	5	10, 19, 26, 44	23.8 (3.3)	14.2 - 37.4	0.00
Yan *et al.* (2000)	x[7]	29	24, 25, 27, 24	24.0 (4.0)	3.8 - 39.9	0.04
Yates *et al.* (2000)	x[8]	95	25, 25, 25, 25	25.6 (3.3)	6.0 - 40.2	0.12
Mills *et al.* (2003)	x[9]	100	25, 25, 25, 25	23.7 (3.2)	7.2 - 38.5	0.08
Mills *et al.* (2003)	x[10]	98	25, 25, 25, 25	24.1 (3.1)	9.3 - 39.7	0.08
Mills *et al.* (2003)	x[11]	7	24, 29, 23, 24	24.5 (2.8)	10.4 - 38.5	0.05
Mills *et al.* (2003)	x[12]	49	23, 25, 26, 26	24.4 (3.0)	7.4 - 37.8	0.28
Mills *et al.* (2003)	x[13]	100	25, 25, 25, 25	23.3 (3.2)	2.2 - 35.4	0.00
Mills *et al.* (2003)	x[14]	98	25, 25, 25, 25	22.4 (3.1)	2.1 - 34.0	0.00
Mills *et al.* (2003)	x[15]	7	24, 29, 23, 24	23.1 (4.2)	2.6 - 36.7	2.62
Hindrichsen *et al.* (2005)	x[16]	100	25, 25, 25, 25	23.8 (3.3)	6.7 - 39.2	0.07
Yan *et al.* (2005)	x[17]	100	25, 25, 25, 25	23.2 (2.6)	1.0 - 28.0	0.00
Ellis *et al.* (2007)	x[18]	100	25, 25, 25, 25	17.5 (2.5)	4.3 - 29.4	0.01
Yan & Mayne (2007)	x[19]	49	23, 25, 26, 26	19.7 (1.9)	1.4 - 24.5	0.00
Yan & Mayne (2007)	x[20]	42	23, 24, 27, 26	23.2 (2.1)	15.3 - 29.5	1.07
Yan & Mayne (2007)	x[21]	42	23, 24, 27, 26	23.2 (2.9)	3.4 - 31.1	0.15
Mills *et al.* (2009)	x[22]	100	25, 25, 25, 25	20.0 (3.1)	1.7 - 32.7	0.00
Mills *et al.* (2009)	x[23]	7	24, 29, 23, 24	25.0 (3.4)	5.4 - 38.0	0.00
Mills *et al.* (2009)	x[24]	100	25, 25, 25, 25	19.0 (2.5)	0.6 - 24.6	0.00
Mills *et al.* (2009)	x[25]	100	25, 25, 25, 25	23.0 (4.0)	3.5 - 40.9	0.02
Dietary methane value	x[26]	99	25, 25, 25, 25	38.3 (7.5)	2.8 - 74.3	-

Table 7 shows that several equations gave predictions below the dietary methane value x[26], such as x[1], x[2], x[3], x[6], x[13], x[14], x[17], x[19], x[22], x[23] and x[24].

Even though the methane output predictions for equation x[6] are all below the dietary methane value, this equation has a poor data coverage (5% of weekly records) and a skewed distribution of prediction records across the range of DM intakes in the dataset compared to other equations, shown in Table 7 (10%, 19%, 26% and 44% of records across DM intake range of 1.4 to 35.4 kg/day). Equation x[6] lacks predictions below 12.8 kg DM intake, and Fig 1 shows that the second order polynomial trendline for this equation goes above the dietary methane value at low DM intakes. Other equations which do not produce methane output predictions across the whole range of DM intakes in the dataset from 1.4 to 35.4 kg/day are x[11], x[15] and x[23] (all cover the range from 3.5 to 33.7 kg/day for DM intake respectively).

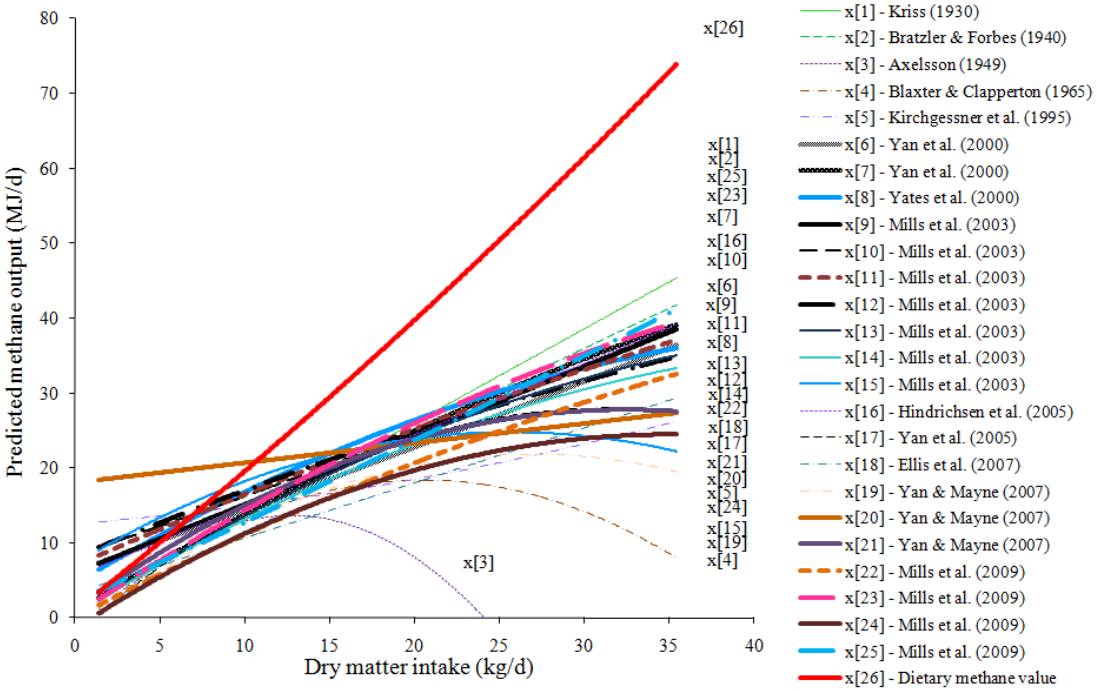

Fig. 1. Average methane output polynomial trendlines for methane output predictions by equations x[1] to x[25] and in comparison to dietary methane values x[26] across the range of daily dry matter intakes seen in the dataset.

Daily DM intake has a high association with many of the equations. Daily DM intake was positively correlated with several other input variables used in equations such as live weight ($r = 0.28$, $P < 0.001$), daily milk yield ($r = 0.60$, $P < 0.001$) and, as expected,

highly correlated with GE, DE and metabolisable energy (ME) intake (r = 0.97, 0.97, 0.98, all $P < 0.001$ respectively). The R-squared values for second order polynomial trendlines for the association of predicted methane output and daily DM intake (Fig. 1) were high in the majority of cases, with values ranging from 0.92 to 1.0, except for equations x[4], x[5], x[15], x[20] whose values were 0.79, 0.78, 0.20 and 0.64 respectively. The variation in R-squared values highlights the emphasis put on other input variables in prediction equations, such as equations x[4], x[5], x[15] and x[20] which use digestibility of GE at maintenance, daily milk yield, dietary starch to ADF content and live weight, than daily DM intake. Table 8 shows that the rank correlations for equations x[3], x[4], x[5], x[15] and x[20] are consistently below 0.70 when methane predictions from each equation are ranked against each other; whereas the remaining prediction equations give high and positive rank correlations.

Table 8. Rank correlation coefficients for the 26 methane output prediction equations used in the study

x[1]	1.00																		
x[2]	0.94	1.00																	
x[3]	-0.96	-0.88	1.00																
x[4]	0.30	0.41	-0.18	1.00															
x[5]	0.65	0.60	-0.69	0.09	1.00														
x[6]	0.91	0.72	-0.91	-0.05*	0.49	1.00													
x[7]	0.90	0.90	-0.83	0.59	0.50	0.99	1.00												
x[8]	0.81	0.82	-0.77	0.48	0.46	0.87	0.90	1.00											
x[9]	1.00	0.94	-0.96	0.30	0.65	0.91	0.90	0.81	1.00										
x[10]	0.97	0.88	-0.94	0.16	0.64	0.87	0.80	0.73	0.97	1.00									
x[11]	0.96	0.91	-0.95	0.12*	0.53	0.81	0.87	0.89	0.96	0.93	1.00								
x[12]	0.81	0.82	-0.77	0.46	0.40	0.88	0.92	0.96	0.81	0.72	0.90	1.00							
x[13]	1.00	0.94	-0.96	0.30	0.65	0.91	0.90	0.81	1.00	0.97	0.96	0.81	1.00						
x[14]	0.97	0.88	-0.93	0.17	0.63	0.87	0.80	0.73	0.97	1.00	0.93	0.71	0.97	1.00					
x[15]	0.13	0.10	-0.12	-0.12*	-0.30	0.62	-0.17**	0.34	0.13	0.06	0.30	0.55	0.13	0.06	1.00				
x[16]	1.00	0.94	-0.96	0.30	0.65	0.91	0.90	0.81	1.00	0.97	0.96	0.81	1.00	0.97	0.13	1.00			
x[17]	1.00	0.94	-0.95	0.31	0.63	0.91	0.89	0.81	1.00	0.97	0.95	0.81	1.00	0.97	0.13	1.00	1.00		
x[18]	1.00	0.94	-0.96	0.30	0.65	0.91	0.90	0.81	1.00	0.97	0.96	0.81	1.00	0.97	0.13	1.00	1.00	1.00	
x[19]	0.91	0.90	-0.83	0.49	0.46	0.87	0.94	0.93	0.91	0.83	0.96	0.95	0.91	0.84	0.43	0.91	0.91	0.91	1.00
x[20]	0.51	0.53	-0.54	0.57	0.64	0.40	0.58	0.38	0.51	0.49	0.53	0.38	0.50	0.48	-0.53	0.51	0.49	0.51	0.43	1.00
x[21]	0.83	0.78	-0.74	0.60	0.39	0.92	0.87	0.70	0.83	0.77	0.82	0.70	0.83	0.78	-0.21	0.83	0.83	0.83	0.79	0.69
x[22]	1.00	0.94	-0.96	0.30	0.65	0.91	0.90	0.81	1.00	0.97	0.96	0.81	1.00	0.97	0.13	1.00	1.00	1.00	0.91	0.51
x[23]	1.00	0.97	-0.99	0.004^{NS}	0.58	0.81	0.85	0.86	1.00	0.99	0.95	0.83	1.00	0.99	0.12	1.00	1.00	1.00	0.93	0.54
x[24]	0.99	0.92	-0.94	0.31	0.63	0.91	0.87	0.79	0.99	0.97	0.95	0.78	0.99	0.97	0.13	0.99	0.99	0.99	0.89	0.50
x[25]	0.99	0.92	-0.95	0.26	0.65	0.89	0.86	0.75	0.99	0.97	0.94	0.75	0.99	0.97	0.09	0.99	0.98	0.99	0.86	0.51
x[26]	0.97	0.91	-0.95	0.24	0.69	0.86	0.82	0.68	0.97	0.95	0.90	0.69	0.97	0.95	0.03^{NS}	0.97	0.97	0.97	0.81	0.52
	x[1]	x[2]	x[3]	x[4]	x[5]	x[6]	x[7]	x[8]	x[9]	x[10]	x[11]	x[12]	x[13]	x[14]	x[15]	x[16]	x[17]	x[18]	x[19]	x[20]

x[21]	1.00					
x[22]	0.83	1.00				
x[23]	0.82	1.00	1.00			
x[24]	0.81	0.99	1.00	1.00		
x[25]	0.80	0.99	0.99	0.99	1.00	
x[26]	0.79	0.97	0.97	0.97	0.98	1.00
	x[21]	x[22]	x[23]	x[24]	x[25]	x[26]

All $P < 0.001$ unless shown. NS = not significant, * $P < 0.05$, ** $P < 0.01$.

Comparing equations across all assessment criteria showed that equations x[1], x[13], x[14], x[22] and x[24] gave reliable methane output predictions based on criteria one to five. Equations x[1], x[13], x[14], x[22] and x[24] are all dependent on DM intake, with x[14] and x[24] using ME intake and GE intake respectively as the input variable, with equations only varying in there ability on average to predict methane output, which were in this study 25.1 ± 4.3, 23.3 ± 3.2, 22.4 ± 3.1, 20.0 ± 3.1 and 19.0 ± 2.5 MJ/day respectively (Table 6). Differences between the predicted methane outputs of these equations are particularly apparent at higher DM intakes (Fig. 2).

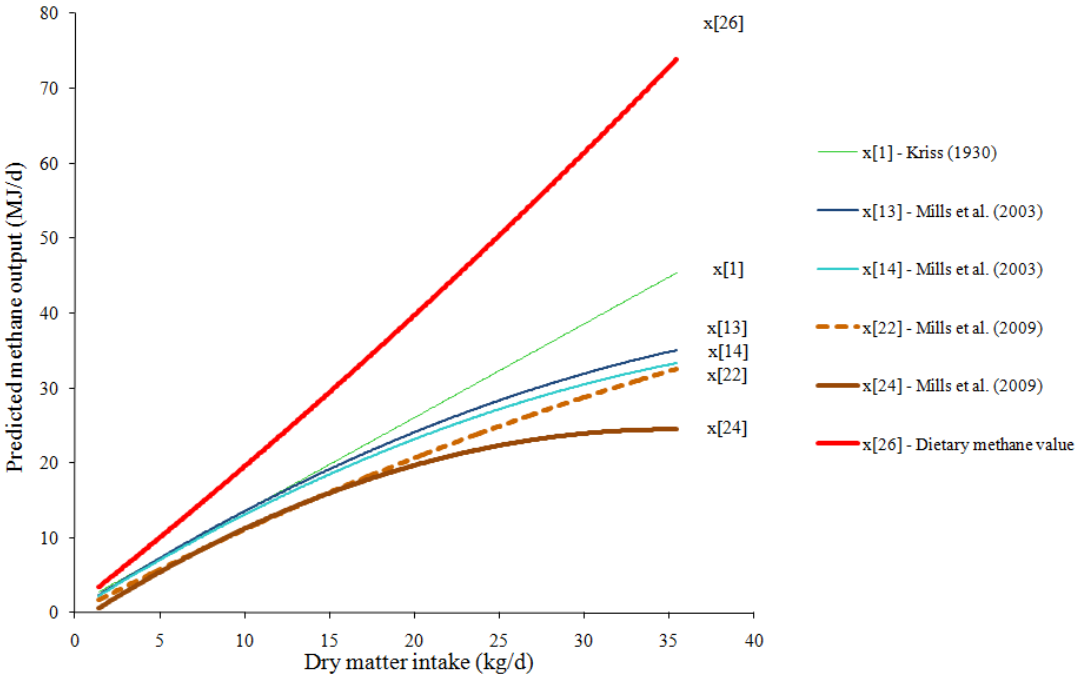

Fig. 2. Average methane output polynomial trendlines for methane output predictions by equations x[1], x[13], x[14], x[22] and x[24] and in comparison to dietary methane values x[26] across the range of daily DM intakes seen in the dataset.

Equations x[1], x[13] and x[14] have been assessed and performed well in validation studies (criterion 6), with R-squared values ranging from 0.56 to 0.66 (Table 6). However, prediction equations x[22] and x[24] were developed on a large and broader range of production values than equations x[1], x[13] and x[14].

2.5 Discussion and conclusions

The cows in this study had a broad range of daily milk yields, daily DM intakes and live weights. The maximum values for milk yield, DM intake and live weight were higher than cows on experiments where methane prediction equations have been developed, with values ranging from 0 to 66 kg/day, 1 to 35 kg/day and 388 to 919 kg respectively. It is well established from past studies that the success or suitability of a statistical prediction equation is dependent on the range of values that the equation was developed on, which includes high milk yielding animals with high feed intakes as well as those with relatively low intakes. Therefore before applying a methane output prediction equation to this kind of dataset, it was important to indentify methane prediction equations that could be used outside the range of values from which they were developed, in the absence of methane measurements on these animals. This study used a range of criteria to evaluate the suitability of prediction equations using the input values available, and does not show that the predictions obtained by different equations are wrong but merely identifies the appropriateness of using equations from the literature on a dataset of this kind.

In the study by Mills *et al.* (2003), the milk yields, DM intakes and live weights of the experimental cows ranged from 14 to 60 kg/day, 13 to 28 kg/day and 494 to 826 kg respectively. However, Mills *et al.* (2009) extended the range of input values seen in Mills *et al.* (2003) using more datasets from more experiments, and lowered the minimum milk yields, DM intakes and live weights to 1 kg/day, 2 kg/day and 173 kg respectively and created a new set of prediction equations using a larger dataset. At lower DM intakes there are several prediction equations which give similar methane output results. However, since it is well established now that methane output per unit DM intake is non-linear, and the non-linear prediction equations of Mills *et al.* (2003) and Mills *et al.* (2009) that include functions of nutrient intake that pass through the origin are based on cows with a similar daily milk yield, DM intake and live weight to the Langhill cows, then it would be appropriate to suggest that these equations may be most suitable for the Langhill cows. The non-linear equations of Mills *et al.* (2003) that

include DM intake and ME intake as input variables show similar results to each other in this study and in past validation studies (Ellis *et al.* 2007). However, the equations developed by Mills *et al.* (2009) use a broader range of input values to their previous study (Mills *et al.* 2003). This study found that the non-linear equation based on DM intake and another using GE intake as well as DM intake by Mills *et al.* (2009) could reliably be used on data that shows a similar range of production values to the Langhill herd i.e. commercial dairy systems. However, as yet these equations have not been validated in other studies.

In conclusion, several methane prediction equations give similar results within a range of about 5-15 kg DM intake but outside this range equations start to show more variation and in some cases give unrealistic results. A great deal of variation in the predicting ability of equations was seen in this study, which may be compromised in some cases by the complexity and availability of input variables. This work highlights that when a particular study looks to apply a methane prediction equation to a dataset, consideration should be given to its suitability. There are opportunities for future work to further develop methane output prediction equations using a broader range of input values.

Chapter 3 Effect of breeding for milk yield, diet, and management on enteric methane emissions from dairy cows[2]

3.1 Summary

Enteric methane production from livestock is an important source of anthropogenic GHG emissions. The aims of this study were to: 1) assess the effect of long-term breeding for kilograms of milk fat plus protein production and 2) investigate the influence of lactation number, genetic line and diet on predicted enteric methane emissions of Holstein-Friesian dairy cows. Data from the Langhill Holstein-Friesian dairy herd were obtained from November 1990 to October 2007. Restricted Maximum Likelihood (REML) was used to assess the effects of lactation number, genetic line and diet on the predicted enteric methane output of lactating and dry cows. A non-linear equation based on metabolisable energy (ME) intake was used to predict daily enteric methane output. This study found that selection for kilograms of milk fat plus protein production, non-grazing low forage diets and maintaining persistently high-yielding older cows can reduce a cow's enteric methane emissions per kg milk by up to 12%, on average. Comparing the first five years to the most recent five years of the study period showed that large savings of 19% and 23% in enteric methane per kg milk were made in cows selected for milk fat plus protein or selected to remain close to the average genetic merit for milk fat plus protein production for all animals evaluated in the UK respectively. Additionally, management to minimise the length of the drying off period can help reduce enteric methane emissions during a cow's lactation period.

Key Words: Dairy cow, methane prediction, lactating, dry, housed, grazing.

[2] Published in Animal Production Science (Bell *et al.*, 2010a).

3.2 Introduction

Livestock contribute significantly to global anthropogenic methane emissions, with about 80% of their methane emissions coming from enteric fermentation (Steinfeld *et al.*, 2006). Prediction equations offer a practical way for estimating the methane output from dairy cows in the absence of direct, easy and accurate measures. The important input variables for these equations are generally dry matter (DM) intake, and nutrient intake and digestibility of the diet. The feed intake of animals at pasture can also be estimated using prediction techniques, as discussed by Ulyatt *et al.* (2002), based on the energy requirements of an animal. Key components for estimating pasture DM intake are milk yield, milk composition and live weight.

Over the last 25 years dairy cow milk yields have increased more rapidly than DM intake, due to increased use of high energy dense diets resulting in improved efficiencies of rumen fermentation and feed digestibility (Eastridge, 2006). The rate of fermentation and digestibility of the diet can help reduce methane production by increasing the passage of food through the gut (Johnson and Johnson, 1995), which is generally faster for concentrates than for forages such as grass (Tamminga *et al*., 2007). As reviewed by Moss *et al.* (2000), the carbohydrate source within a diet will influence the methane producing capabilities of the food consumed. Several studies (Holter and Young, 1992; Moss *et al*., 2000; Lovett *et al*., 2006; Yan and Mayne, 2007) have shown the savings in enteric methane output per kg milk that can be made by supplementing diets with concentrates, improving feed quality (in terms of neutral detergent fibre, crude protein and ME content) and improving the overall milk production of the animal.

Bauman *et al.* (1985) found that improvements in production efficiency of cows, i.e. the ratio of milk yield to resource input, are due to a dilution of maintenance requirement. High milk producing cows, with higher feed intakes and enteric methane outputs are associated with lower methane outputs per kg milk (Chagunda *et al.*, 2009). If the dairy industry is to meet the growing global demand for dairy products, ways to minimise

methane emissions per unit product in a sustainable way will become increasingly important. Capper *et al.* (2009) discussed the need to adopt management practices and technologies that improve productive efficiency if the demand for dairy products is to continue to be satisfied while resource use and environmental impact are minimised. Bauman *et al.* (1985) found that selecting dairy cows on increased productive efficiency with regard to maintenance energy requirements, ME use for milk synthesis, and digestion and nutrient absorption, showed less potential than that associated with nutrient partitioning and feed intake. There is potential for reducing methane emissions by selecting dairy and beef animals with improved feed efficiency (Hegarty *et al*., 2007).

The objectives of this study were: 1) to assess the effect of long-term breeding for kilograms of milk fat plus protein production and 2) investigate the influence of lactation number, genetic line and diet on enteric methane emissions of Holstein-Friesian dairy cows from the Langhill herd.

3.3 Materials and Methods

3.3.1 Data

The data used in this study were collected from November 1990 to October 2007. The data are described in Section 1.3.3, which included lactating and dry cows. Lactating cows were fed a diet containing a low or high proportion of forage, and when non-lactating, dry cows received diets D1 to D5. Pasture DM intake was also determined for lactating and dry cows (D6). The average number of days that lactating cows spent at pasture per lactation at Farms 1 and 2 were 107 ± 52.0 days and 160 ± 72.9 days respectively. The number of days spent on diets D1 to D6 were 20.6 ± 8.9, 32.3 ± 3.7, 43.3 ± 11.1, 12.6 ± 6.2, 13.7 ± 5.5, 43.9 ± 27.2 days (mean ± s.d.). Table 9 shows the average daily milk yield ranged from 0 to 66 kg/day, DM intake ranged from 1.4 to 35 kg/day and live weights in the dataset ranged from 366 to 919 kg, for cows indoors. The data from cows that temporarily lost their appetite were also included, hence a minimum

daily DM intake of 1.4 kg/day. Table 9 also shows the chemical composition of the food fed to lactating and dry cows.

Table 9. Average milk yields, live weights, dry matter intakes and chemical composition of food consumed by lactating and dry housed cows

		Mean (s.d)	Range
Milk yield	kg/day	27.7 (8.6)	0 - 65.7
Dry matter intake	kg/day	19.3 (3.7)	1.4 - 35.4
Live weight	kg	637 (75)	366 - 919
Metabolisable energy	MJ/kg DM	11.6 (0.5)	8.1 - 12.9
Dry matter	g/kg DM	340 (58)	221 - 556
Acid detergent fibre (ADF)	g/kg DM	226 (34)	170 - 365
Neutral detergent fibre	g/kg DM	409 (67)	285 - 781
Sugar	g/kg DM	25 (15)	1 - 67
Starch	g/kg DM	125 (49)	0 - 232
Crude protein	g/kg DM	176 (20)	63 - 214
Forage ADF	g/kg DM	303 (139)	117 - 915
Forage in total dry matter	%	78.1 (10.7)	38.8 - 100
Total mixed ration in diet	%	95.4 (2.7)	32.5 - 100

3.3.2 Prediction equations

The daily enteric methane output was predicted from ME intake using the non-linear equation of Mills *et al.* (2003) (Table 10). This equation was identified in a previous study (Bell *et al.*, 2009, which has subsequently been updated as shown in Chapter 2) as suitable for the wide range of DM intake values seen in the Langhill herd data. Enteric methane predictions for housed and grazing cows were only made on days when DM intake was known, either measured for housed animals or predicted when grazing as described below and shown in Table 10. Daily enteric methane output per kg milk was determined on days when both DM intake and milk yield were known, which meant that 2% of the weekly average values for housed cows were lost due to there being no milk yield recorded on the same day as DM intake being measured. The DM intake prediction models shown in Table 10 by the NRC (2001) and Halachmi *et al.* (2004) were compared to identify the better one for predicting DM intake at pasture. Halachmi *et al.* (2004) suggested that their DM intake prediction model was an improvement on the NRC (2001) model, which is based on many years of research (e.g. Roseler *et al.*, 1997). Daily DM intake predictions from these models were compared with 8,422

measured DM intakes from March 2005 to October 2007 for cows that were housed throughout the year. The model that was identified as the more accurate predictor of DM intake, by comparing observed against predicted DM intakes, was then used along with the energy balance model (**EB** model) to determine daily DM intake at pasture from the dataset.

Table 10. Prediction equations used in this study

Source	Equation
Mills *et al.* (2003)	Methane (MJ/day) = $45.98 - (45.98 + 0) \times e^{[-0.003 \times \text{ME intake}]}$
EB - 1*	ME maintenance = $[0.53 \times (\text{LWGT} / 1.08)^{0.67} + 0.00947 \times \text{LWGT}] / 0.72$
EB - 2*	ME milk = $(0.0406 \times \text{MF (g/kg)} + 1.509 \times \text{MY}) / 0.62$
EB - 3*	ME pregnancy = $0.025 \times [\text{CLWGT} \times (10^{151.665 - 151.64 \times eT}) \times (0.0201 \times e^{T})] / 0.133$; $T = -0.0000576 \times \text{CD}$
EB - 4*	ME live weight change = 32 (gain) and 26 (loss) MJ/kg
Energy balance (EB)	Pasture DMI (kg) = [(ME maintenance + ME milk + ME pregnancy + ME live weight change) – ME intake] / ME pasture
NRC (2001)	DMI (kg/day) = $0.372 \times [0.4 \times \text{MY} + 15 \times (\text{MF} / 100) \times \text{MY}] + [0.0968 \times \text{LWGT}^{0.75}] \times 1 - e^{(-0.192 \times \text{WOL}) + 3.67}$
Halachmi *et al.* (2004)	DMI (kg/day) = $[23.52 + 0.34 \times (\text{MY} \times 100) / \text{LWGT} - 0.49 \times (\text{MY}^{-1} \times 100) / \text{LWGT}^{-1} + 0.37 \times (\text{MY}^{-2} \times 100) / \text{LWGT}^{-2} - 0.3 \times \text{LWGT} / 100 - 18.86 \times \text{LWGT}^{-1} / \text{LWGT} - 0.25 \times \text{MF}] / 100 \times \text{LWGT}$

EB 1 to 4 are used to calculate energy balance (EB). * AFRC (1993) with efficiencies of utilisation of ME for maintenance (0.72, EB – 1) and milk synthesis (0.62, EB – 2) obtained from MAFF (1975). ME = metabolisable energy (MJ/day); DMI = dry matter intake (kg/day); MY = milk yield (kg/day); MF = milk fat composition (%); LWGT = cow live weight (kg); CLWGT = calf birth weight (kg); CD = days since conception; WOL = week of lactation.

The EB model (developed from AFRC (1993) and MAFF (1975)) assumes that the energy required for maintenance, milk production, pregnancy and live weight change comes from the feed consumed. Enteric methane output predictions for cows at pasture assumed a constant chemical composition of their DM intake as described in Section 1.3.3. The average calf birth weights of the lactating and dry grazing cows where the EB model was used were 47.5 ± 8.2 kg and 46.6 ± 8.1 kg respectively. The energy balance calculations for lactating cows used single weekly cow live weights prior to

June 2002 and weekly averages after June 2002, and dry cows had single weekly live weights from June 2004.

3.3.3 Records

During the study period 223,616 daily DM intake records were recorded from 960 lactating housed cows (91,220, 61,595 and 70,801 for lactations 1, 2 and 3 or 3+ respectively) and 3,406 from 71 dry housed cows (1,640, 906 and 860 for lactations 1, 2 and 3 or 3+ respectively). Weekly average daily DM intake, daily milk yield, daily ME intake and daily predicted enteric methane output (expressed as MJ/day, % of ME intake and MJ/kg milk) were used for the analyses. There were 62,386 weekly average records for all housed cows, of which Low Forage Farm 1: 19,914, High Forage Farm 1: 19,535, Low Forage Farm 2: 15,575, High Forage Farm 2: 6,768 and dry cows: 594. There were fewer weekly records for housed High Forage cows at Farm 2 than for Low Forage cows as the former received summer grazing.

3.3.4 Statistical analysis

The data were analysed using Genstat Version 11.1 (Lawes Agricultural Trust, 2009) and Restricted Maximum Likelihood (REML). A linear mixed model was used to compare weekly averages for DM intake, milk yield, live weight, ME intake and predicted enteric methane output (MJ/day, % of ME intake and MJ/kg milk). In previous studies on the Langhill cows, diet, genetic line, lactation number, percentage North American Holstein genes, live weight, age at calving, week of lactation, year and month of calving were added as fixed effects (Veerkamp *et al.*, 1994; Pryce *et al.*, 1999; Coffey *et al.*, 2001; Chagunda *et al.*, 2009). In the present study neither age at calving nor percentage North American Holstein genes were found to have a statistically significant effect after fitting lactation number into the model, which is consistent with the results of Pryce *et al.* (1999). Cow live weight was not included in the statistical

model as it is an input variable of the EB and NRC models. Cow identity was added as a random effect to allow for covariance between subsequent lactations of the same cow.

The following statistical model was used to evaluate the effect of lactation number, genetic line and diet:

$$Y_{ijklm} = \mu + Yr_i + M_j + L_k + D_l \times G_m + \beta(W)_{ijklm} + C_{ijklm} + E_{ijklm}$$

where, Y_{ijklm} = DM intake (kg/day), milk yield (kg/day), ME intake (MJ/day), predicted methane output (MJ/day, % of ME intake and MJ/kg milk); μ = overall mean; Yr_i = fixed effect of year of calving; M_j = fixed effect of month of calving; L_k = fixed effect of lactation number (1, 2 and 3 or 3+); D_l = fixed effect of diet (Low Forage and High Forage at Farm 1 or 2, lactating at pasture and dry cow diets D1 to D6); G_m = fixed effect of genetic line (Control or Select); $\beta(W)_{ijklm}$ = regression effect of weeks since calving; C_{ijklm} = random effect of cow; E_{ijklm} = random error term.

Wald tests, which use a χ^2 distribution, were used to examine the level of significance of the differences within the fixed effects. The profiles of predicted enteric methane output and enteric methane output per kg milk were shown for weeks 1 to 38 post calving and were generated by the interaction between lactation number with weeks since calving, and diet × genetic line with weeks since calving (Fig. 3 to 6). Polynomials of order 6 were used to model each profile. The effect of the breeding experiment on enteric methane output per kg milk over time was assessed by comparing the average predicted value for the first five years of the study period to the most recent five years for Control and Select genetic lines. For this comparison the fixed effect of year of calving in the statistical model was replaced by the interaction between genetic line and farm.

Spearman's rank correlation was used to test the association between actual DM intake and DM intake prediction models.

Observed actual DM intake (O_i) and predicted DM intake (P_i) values were also compared using mean square prediction error (MSPE) for all observations (n):

$$\text{MSPE} = \sum_{i=1}^{n} (O_i - P_i)^2/n,$$

Square root of the MSPE (RMSPE), expressed as a percentage of the observed mean DM intake, gives an indication of the overall prediction error. Significance was attributed at $P < 0.05$.

3.4 Results

3.4.1 Daily enteric methane output predictions at pasture

Testing the use of DM intake prediction models for cows at pasture showed that the NRC (2001) model had a positive and higher correlation (r = 0.523; $P < 0.001$) and a better precision of prediction (RMSPE = 20.3%) of the measured DM intakes than the Halachmi *et al.* (2004) model (r = 0.151; $P < 0.001$; RMSPE = 22.6%). Daily DM intake predictions ranged from 5.0 to 32.7 kg/day (19.0 ± 3.3 kg/day), -16.5 to 48.8 kg/day (18.3 ± 3.2 kg/day) and 7.3 to 29.7 kg/day (21.3 ± 2.8 kg/day) for measured daily DM intake, Halachmi *et al.* (2004) and NRC (2001) models respectively. The NRC (2001) was therefore used to predict DM intake for lactating cows at pasture.

In addition to the NRC (2001) model the EB model was used to test its suitability, as it could be used on dry cows. The NRC (2001) and EB models were positively correlated (r = 0.468, $P < 0.001$) and the average predicted daily DM intakes ranged from 7.9 to 30.7 kg/day (19.7 ± 2.6 kg/day) and 8.5 to 78.9 kg/day (21.1 ± 4.8 kg/day) respectively.

There were more weekly average DM intake records produced using the NRC (2001) model than the EB model; 18,942 DM intake records from 752 cows (6,859, 5,462 and 6,621 for parities 1 to 3 or 3+ respectively) for the NRC (2001) model compared to 10,515 records from 586 cows (2,656, 3,530 and 4,329 for lactations 1 to 3 or 3+ respectively) for the EB model. Of these records, 9,400 and 9,542 were for the NRC (2001) model and 5,862 and 4,653 were for the EB model at Farms 1 and 2 respectively. Comparing the average DM intake predictions for lactating cows at Farm 1 and Farm 2 at pasture using both models, showed that the NRC (2001) model gave a similar range of values at both farms whereas the EB model had a broader range of values and a larger standard deviation at Farm 1 compared to Farm 2 (NRC (2001) model at Farm 1 = 7.9 to 29.0 kg/day, mean of 19.1 ± 2.4 kg/day and Farm 2 = 9.1 to 30.7 kg/day, mean of 20.3 ± 2.6 kg/day; EB model at Farm 1 = 9.8 to 78.9 kg/day, mean of 21.2 ± 5.4 kg/day and Farm 2 = 8.5 to 38.4 kg/day, mean of 21.0 ± 3.8 kg/day). There were 2,027 weekly DM intake records (539, 483 and 1,005 for lactations 1 to 3 or 3+ respectively) from 212 dry cows at pasture using the EB model. Predicted daily DM intakes ranged from 5.9 to 51.3 kg/day (15.7 ± 5.9 kg/day) for dry cows at pasture. The predicted daily enteric methane output of lactating cows at pasture ranged from 11.9 to 42.2 MJ/day (22.4 ± 3.3 MJ/day) for the EB model and 10.8 to 29.6 MJ/day (21.5 ± 2.1 MJ/day) for the NRC (2001) model, and for the dry cows from 7.8 to 36.9 MJ/day (17.5 ± 4.6 MJ/day) for the EB model. This compares to predicted average daily enteric methane outputs ranging from 2.0 to 37.6 MJ/day (22.5 ± 3.1 MJ/day) for lactating housed cows and 2.3 to 25.6 MJ/day (11.9.0 ± 4.0 MJ/day) for dry housed cows over the study period.

3.4.2 Effect of lactation number, diet and genetic line

There was a maximum of 83,354 weekly records (from 1,191 cows) across lactations, diets and genetic lines during the study period, of which 62,386, 18,984 and 2,026 weekly records were for housed cows, and lactating and dry cows at pasture, respectively. Weekly averages for DM intake, milk yield, live weight, ME intake and predicted enteric methane output (MJ/day, % of ME intake and MJ/kg milk) were

compared across lactations, diets and genetic lines. Table 11 shows that there were significant differences in DM intake, milk yield, live weight, ME intake, predicted enteric methane output as a % of ME intake and per kg milk (all $P < 0.001$) for cows of different lactation number, genetic line, diet and the interaction between diet and genetic line.

Table 11. Predicted mean dry matter intake, milk yield, live weight, metabolisable energy intake (MEI), methane output as a % of ME intake and per kg milk for different lactations, diets and genetic lines

Lactation	Dry matter intake kg/day	Milk yield kg/day	Live weight kg	MEI MJ/day	Methane % of MEI	Methane MJ/kg milk
1	14.7	22.5	587	149	11.2	1.00
2	17.1	26.4	629	177	10.8	0.96
3 or 3+	17.8	27.7	661	184	10.7	0.97
SED	0.03***	0.06***	0.6***	0.4***	0.01***	0.004***
Diet						
LF Farm 1	21.3	27.6	640	256	9.6	0.94
HF Farm 1	19.3	23.8	634	226	10.0	1.01
LF Farm 2	19.7	28.9	615	234	9.9	0.91
HF Farm 2	17.7	24.1	615	192	10.5	0.96
Lactating at pasture	20.0	24.6	599	216	10.2	1.00
D1	18.9	24.0	632	224	10.1	1.04
D2	15.0	-	623	139	11.4	-
D3	11.5	-	639	84	12.2	-
D4	11.4	-	628	65	12.6	-
D5	11.5	-	638	72	12.4	-
Dry at pasture (D6)	15.2	-	620	162	11.0	-
SED	0.4***	0.3***	5.9***	4.4***	0.06***	0.02***
Genetic line						
Control	15.9	23.3	628	164	11.0	1.04
Select	17.1	27.7	623	176	10.8	0.92
SED	0.2***	0.3***	3.5***	2.5***	0.03***	0.02***

LF = Low Forage, HF = High Forage lactating cow diets; D1 to D6 = dry cow diets; SED = standard error of the difference between means; *** $P < 0.001$.

Lactation one cows had the lowest average daily DM intake, milk yield, live weight, ME intake, but the highest predicted enteric methane output as a % of ME intake and per kg milk (Table 11). Over an individual lactation period, 3 or 3+ cows produced about 3% less enteric methane per kg milk than lactation one cows but the profile of Fig. 3 shows that after about 30 weeks since calving they had the highest enteric methane output per

kg milk and lactation one cows then had the lowest. Lactation 3 or 3+ cows had on average a slightly higher daily milk yield per kg DM intake than lactation one cows (1.56 compared to 1.53 kg/kg).

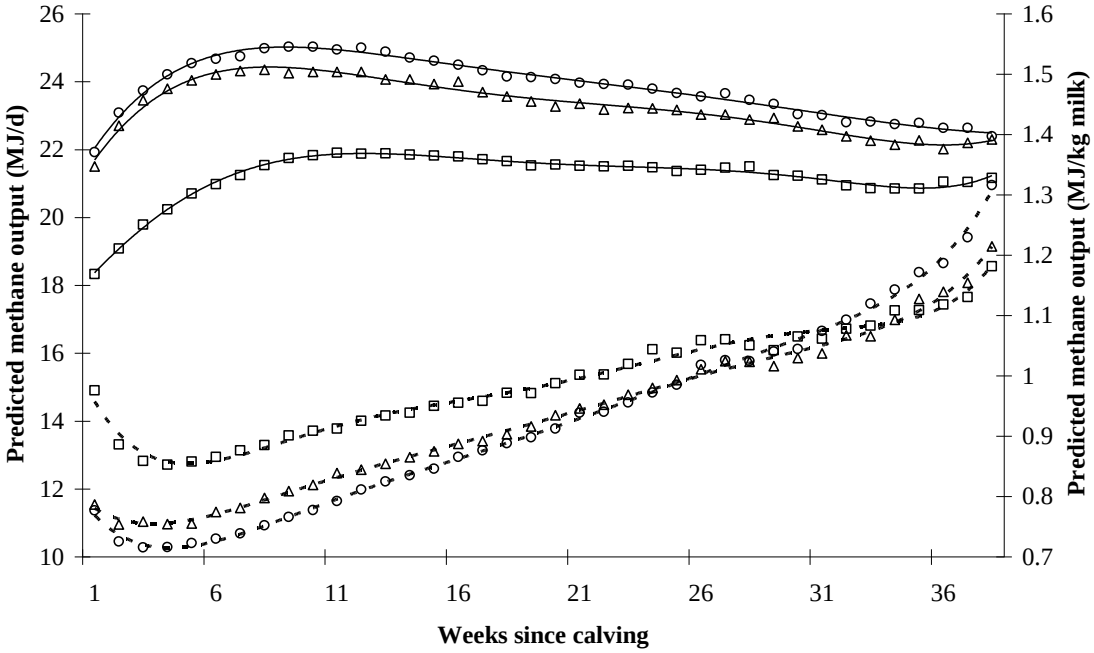

Fig. 3. Predicted methane output (— for MJ and --- for MJ/kg milk) from 1 to 38 weeks since calving for lactation 1 (□), lactation 2 (Δ) and lactation 3 or 3+ (○).

Select genetic line cows had a higher weekly DM intake, milk yield, ME intake, but a lower predicted enteric methane output as a % of ME intake and per kg milk by about 12% (Table 11 and Fig. 4). Select genetic line cows were slightly smaller than Control genetic line cows over the study period (Table 11). Select genetic line cows on average had a higher daily milk yield per kg DM intake (1.62 compared to 1.47 kg/kg) than Control cows. Selection for kilograms of milk fat plus protein over time has reduced the predicted enteric methane output per kg milk of high milking producing cows (Select line) as well as cows selected to be of average genetic merit for milk fat plus protein production. Select cows had predicted enteric methane outputs per kg milk of 0.97 and 0.78 MJ/kg milk compared to 1.17 and 0.90 MJ/kg milk for Control cows at Farm 1 and

Farm 2, respectively (SED = 0.02, $P < 0.01$), which represent a reduction of 19% and 23% between the two periods for Select and Control cows.

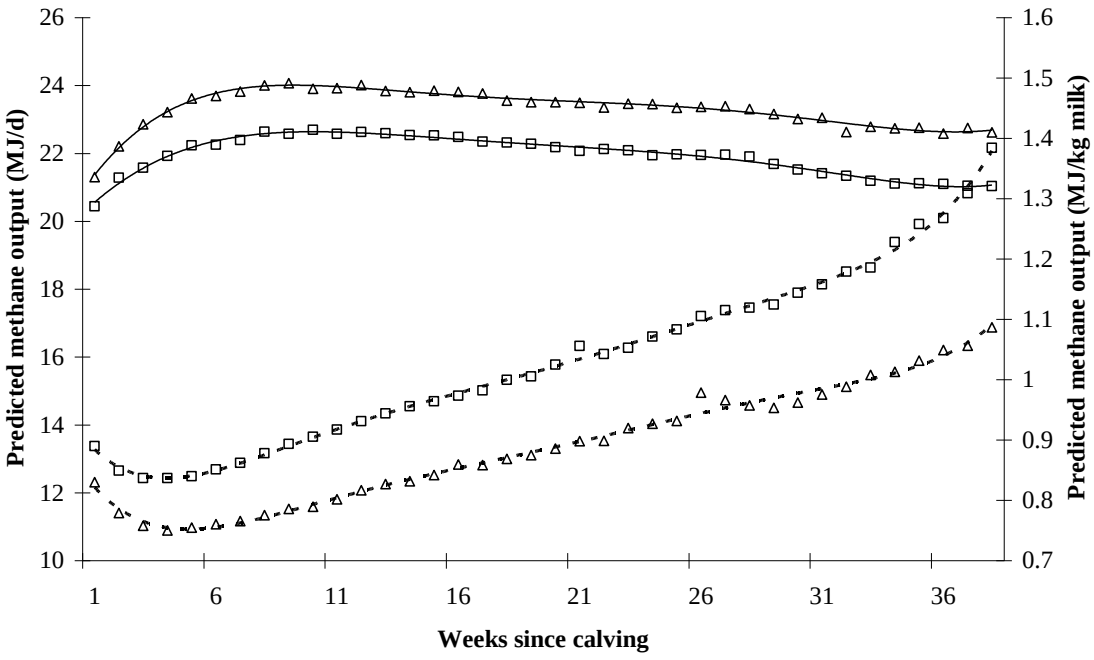

Fig. 4. Predicted methane output (— for MJ and --- for MJ/kg milk) from 1 to 38 weeks since calving for Control (□) and Select (Δ) genetic lines.

In terms of diet, Low Forage cows had a higher daily DM intake, milk yield, ME intake, but had a lower predicted enteric methane output as a % of ME intake and per kg milk than the High Forage fed cows at each respective Farm (Table 11). Low Forage cows at Farm 1 had the lowest predicted enteric methane output as a % of ME intake, compared to other diets. However, the non-grazing Low Forage fed cows at Farm 2 had the lowest enteric methane output per kg milk, which was about 5% lower than High Forage fed animals at the same farm. Non-grazing Low Forage fed cows were more efficient in terms of daily milk yield per kg DM intake (1.47 kg/kg) than cows on a High Forage diet and lactating cows at pasture (ranging from 1.23 to 1.36 kg/kg). The results shown for lactating grazing cows in Table 11 are the averages using the NRC (2001) model for cows across both farms, and the EB model was used for dry cows at pasture. Fig. 5

shows that the EB model and the NRC (2001) model have similar predicted enteric methane output profiles after about week 11 post-calving for grazing animals. In the period up to 11 weeks post-calving, using calculations of a cow's energy balance (EB model) to estimate pasture DM intake, gave a higher estimate of enteric methane output and a different methane output profile compared to the profiles of housed cow diets (Fig. 6) and the NRC (2001) model.

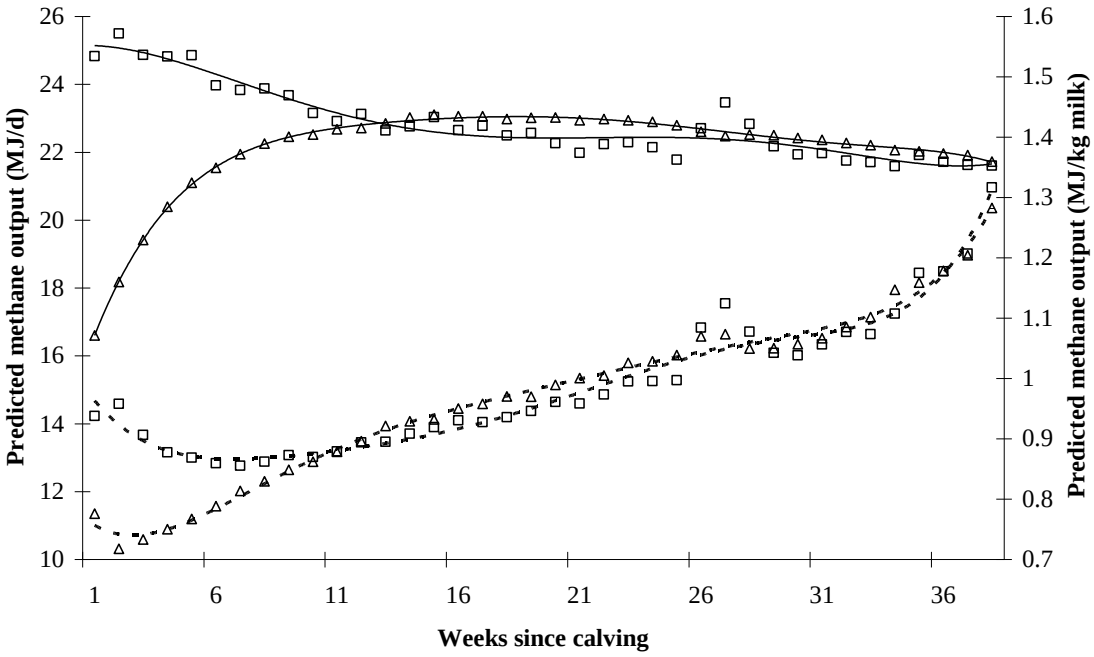

Fig. 5. Predicted methane output (— for MJ and --- for MJ/kg milk) from 1 to 38 weeks since calving for EB model (□) and NRC (2001) model (Δ) for cows at pasture.

The predicted enteric methane output profiles for lactating housed cows on diets at Farm 2 are flatter than the profiles for cows on diets at Farm 1 which peak at about 10 or 11 weeks since calving (Fig. 6). The change in the shape of the methane output profile from Farm 1 to Farm 2 is most likely due to the selection on milk fat and protein production within the Select and Control genetic lines and an improvement in milking persistency. Table 11 shows that cows during their drying off period (diets D2 to D6) had a lower ME intake than lactating housed cows but had a higher proportion of their

ME intake lost as methane at both farms (ranging from 11.0 to 12.6% of ME intake for dry period diets and 9.6 to 10.5% of ME intake for lactating housed diets). Even though predicted DM intakes for dry cows at pasture may appear to be slightly high (15.2 kg/day), the average for all cows is comparable to the D2 drying period diet at Farm 1 (15.0 kg/day). Lactating Control cows at pasture had the highest enteric methane output per kg milk of 1.11 MJ/kg milk, whereas lactating Select cows at pasture are predicted to produce 0.88 MJ/kg milk of enteric methane (Table 12). Select cows appear to be more efficient in terms of predicted enteric methane output as a % of ME intake, kg milk and daily milk yield per kg DM intake (1.29 and 1.17 kg milk/kg DM respectively) than Control cows at pasture.

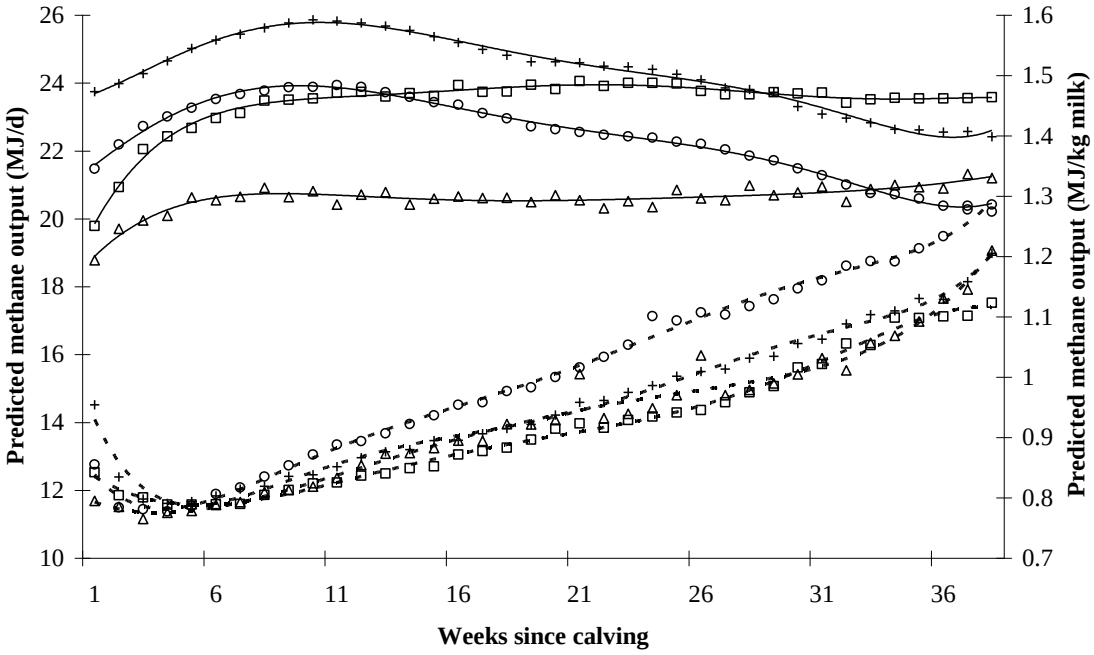

Fig. 6. Predicted methane output (— for MJ and --- for MJ/kg milk) from 1 to 38 weeks since calving for Low Forage Farm 1 (+) and 2 (□), High Forage Farm 1 (○) and 2 (Δ) cows whilst housed.

Non-grazing Low Forage Select cows at Farm 2 had a lower average predicted daily enteric methane output per kg milk than cows on other systems; these cows were

characterised by having a higher daily milk yield per kg DM intake (1.57 kg milk/kg DM) on average (Table 12).

Table 12. Predicted mean dry matter intake, milk yield, live weight, metabolisable energy intake (MEI), methane output as a % of ME intake and per kg milk for diet × genetic line

Diet x genetic line	Dry matter intake kg/day	Milk yield kg/day	Live weight kg	MEI MJ/day	Methane % of MEI	Methane MJ/kg milk
LF Farm 1 Control	20.5	24.7	651	246	9.8	1.00
HF Farm 1 Control	18.7	21.9	639	220	10.1	1.06
LF Farm 2 Control	18.6	25.2	610	221	10.1	1.02
HF Farm 2 Control	16.9	21.9	616	183	10.6	1.05
Lactating at pasture Control	19.2	22.4	606	208	10.3	1.11
D1 Control	18.1	23.5	629	214	10.2	0.97
D2 Control	14.2	-	598	133	11.5	-
D3 Control	11.4	-	645	83	12.2	-
D4 Control	11.1	-	639	64	12.5	-
D5 Control	10.9	-	638	66	12.5	-
Dry at pasture (D6) Control	15.2	-	639	162	11.0	-
LF Farm 1 Select	22.2	30.4	630	267	9.5	0.88
HF Farm 1 Select	19.9	25.6	630	233	9.9	0.95
LF Farm 2 Select	20.8	32.6	620	246	9.8	0.80
HF Farm 2 Select	18.6	26.2	613	200	10.3	0.88
Lactating at pasture Select	20.8	26.8	591	224	10.1	0.88
D1 Select	19.7	24.5	635	234	9.9	1.10
D2 Select	15.8	-	649	146	11.2	-
D3 Select	11.6	-	632	86	12.2	-
D4 Select	11.6	-	617	66	12.6	-
D5 Select	12.1	-	639	78	12.4	-
Dry at pasture (D6) Select	15.3	-	601	162	11.0	-
SED	0.5***	0.4***	8.0***	6.0***	0.08***	0.03***

LF = Low Forage, HF = High Forage lactating cow diets; D1 to D6 = dry cow diets; SED = standard error of the difference between means; *** $P < 0.001$.

However, Low Forage Select cows at Farm 2 had a lower predicted daily enteric methane output as a % of ME intake than other systems, due to their higher DM intake. Control genetic line cows on a pre-drying off D1 diet were predicted to have a lower enteric methane output per kg milk than Control cows on other diets, which reflects the higher daily milk yield per kg DM intake (1.30 kg milk/kg DM) of these cows compared to Select genetic line cows on a D1 diet (1.24 kg milk/kg DM). Control genetic line cows on diets other than the D1 diet, showed that Low Forage fed cows at Farm 1 have the lowest predicted enteric methane output per kg milk and as a % of ME intake, but on

average non-grazing Low Forage fed cows at Farm 2 are more efficient in terms of daily milk yield per kg DM intake (1.35 kg milk/kg DM) than Control cows on other diets (ranging from 1.17 to 1.30 kg milk/kg DM).

3.5 Discussion and conclusions

This study investigated the influence of long-term breeding for milk fat plus protein production, lactation number and diet on predicted enteric methane emissions of Holstein-Friesian dairy cows. Manure is also an important source of methane but this source of emissions was not incorporated into this particular study. The cows in the Langhill herd have a broader range of production values than cows on experiments where enteric methane prediction equations have been developed. However, it is still possible to identify a suitable prediction equation for the range of values seen in the Langhill herd (Chapter 2). The Langhill data enables methane emissions to be extrapolated for a broad range of production values which may be found in commercial dairy herds.

Methane production from enteric fermentation is known to be positively correlated with DM intake and level of production in dairy cattle, but the percentage of dietary GE lost as methane declines with increasing DM intake (Kebreab *et al.* 2006b). In terms of diet, this study found that cows on a low forage feeding system where intakes are particularly high (such as at Farm 1), were the most efficient in terms of proportion of ME intake lost as enteric methane. In contrast, cows during the drying off period and not milking were the least efficient in terms of the proportion of ME intake lost as enteric methane, when DM intake is relatively low. Obviously, the rate of fermentation of the diet and its digestibility, which influence DM intake, are important components for minimising the proportion of energy consumed by the animal that is lost as enteric methane. A high proportion of forage in the diet is associated with a higher enteric methane output per kg milk compared to a more nutrient dense (or low forage) and higher consumed diet which

generally ferments faster in the rumen (Johnson and Johnson, 1995; Tamminga *et al.*, 2007). However, cereal-based diets can be costly and have additional carbon costs relative to forage produced on-farm, which is not accounted for in this study. Therefore, the quality of the forage with regard to contents such as crude protein, ME and digestibility should be maximised where possible.

Kennedy *et al.* (2003) discussed the limitations of a grazing system for a high milk yielding dairy cow, where nutrient intake at pasture can vary and impair the milk production potential of the animal, particularly during the peak of lactation. Kennedy *et al.* (2003) found that concentrate supplementation of high milk yielding dairy cows at pasture results in a lower rate of pasture DM intake substitution and a higher response in improved milk yield compared to lower milk yielding cows. The difference in enteric methane emissions per kg milk on average between a solely grazing system and a non-grazing system was predicted to be about 9%, which not only reflects the improved feed efficiency and lower proportion of ME intake lost as enteric methane by feeding a high energy dense feed in a non-grazing system but also the increased availability of ME intake for milk production rather than maintenance.

When comparing the use of DM intake prediction models for cows at pasture, it appears in this study that during early lactation the EB model gives a higher estimate of enteric methane output and different profile of predicted methane output compared to housed cow diets and the NRC (2001) model from 1 to 38 weeks since calving. The wider range of values for DM intake predicted at pasture by the EB model for lactating cows at Farm 1 and dry cows at Farm 2 appear to be due to the influence of live weight change and lack of live weight measurements, when compared to periods when live weight was recorded three times a day and a realistic range of values were predicted. The availability and dependency of live weight measures may explain the error associated with the NRC (2001), Halachmi *et al.* (2004) and EB models in predicting pasture DM intake. Caution must be taken when interpreting the cow live weight results between

farms as lactating cows at Farm 2 were weighed three times per day compared to a single weekly measurement at Farm 1 or when cows were being dried off at either farm. Yan *et al.* (2003) compared models for predicting the energy balance of dairy cows, and reported that live weight change is inappropriate for determining the total energy requirement of a lactating dairy cow; however, this was based solely on weekly live weight measurements rather than averaged weekly measurements. Also, this study did not take into account any fluctuations in the quality of the grass consumed, but assumed a good quality sward. However, it was felt that this necessary approximation did not introduce significant error because grazing was intensively managed for quality and only used when available during the summer months. Using energy requirements to predict enteric methane production at pasture can produce realistic results as discussed by Ulyatt *et al.* (2002) and shown by the predictions for lactating cows at pasture, as long as averaged weekly live weights and analysis information of pasture are available.

Veen (2000) stated that the digestibility of forage in dairy systems has limited potential for improvement as this is already high, whereas the largest contribution to reducing methane emissions from dairy cows is an increased milk yield per animal. As reported by Yan and Mayne (2007) and Chagunda *et al.* (2009) and seen in this study, an effective way to reduce enteric methane emissions per kg milk in dairy cows is breeding for improved kilograms of milk fat plus protein production (a 12% difference between Control and Select genetic lines, $P < 0.001$), whereby cows partition more of their nutrient intake towards milk production. Over time, selection for kilograms of milk fat plus protein production in both genetic lines has produced large reductions in enteric methane per kg milk of 19% and 23% for Select and Control genetic lines respectively. Notably over time, selecting on milk fat and protein production has resulted in a flattening of the enteric methane output profile of cows on feeding systems at Farm 2 compared to those at Farm 1 and an increased ability to maintain a lower level of enteric methane output per kg milk over a lactation. The flatter enteric methane output profile is most likely due to increased milking persistency. Whilst at pasture, Select genetic line

cows appear to be more efficient in terms of enteric methane as a proportion of ME intake and per kg milk than Control genetic line cows. This study also found that maintaining persistently high yielding older cows, who are able to partition more of their nutrient intake towards milk production, had the potential to produce less enteric methane as a proportion of ME intake and per kg milk (by about 3%) compared to lactation one cows over a lactation period. However, after 30 weeks since calving, older cows had a higher enteric methane output per kg milk than younger cows; genetic progress may also be slowed by maintaining older animals.

Patton *et al*. (2006) showed that gains in efficiencies in terms of milk production can be made by increasing the number of milkings per day, which results in an increase in milk yield but not DM intake. So by changing from a twice per day milking strategy as at Farm 1 to a three times per day system at Farm 2, savings in methane emissions per kg milk will have been made. Overall, the lowest enteric methane output per kg milk was seen in the high yielding cows such as the non-grazing cows bred for improved milk fat and protein production, whereas the animals with the lowest proportion of ME intake lost as enteric methane were cows on a low forage diet with summer grazing and bred for improved milk fat and protein production. However, Chagunda *et al.* (2009) also showed that cows with a high feed intake (such as on a low forage diet) are associated with potentially higher nitrogen excretion per forage hectare compared to cows with lower feed consumption but lower potential nitrogen excretion per kg milk in cows bred for increased milk fat and protein production.

In conclusion, this study found that enteric methane emissions can be reduced by improved productive efficiency whereby cows partition more of their nutrient intake towards milk production, whilst maximising feed efficiency to reduce the proportion of their ME intake lost. Differences in lactation number, genetic line, diet, housing/grazing system, milking persistency and drying off period management all have an impact on the enteric methane output as a % of ME intake and per kg milk from a dairy cow.

Selection for kilograms of milk fat plus protein production, non-grazing low forage diets, maintaining persistently high milk yielding older cows and minimising the drying off period (without compromising the animals health) can all help reduce the enteric methane output as a % of ME intake and per kg milk of dairy cows. Further work will assess system methane emissions including those from manure.

Chapter 4 Effects of genetic line and feeding system on total methane emissions from dairy systems[3]

4.1 Summary

Improving the efficiency of livestock production is a promising way to reduce methane emissions from farming systems. The aims of this study were to: 1) assess effects of lactation number, genetic line and feeding system on estimated enteric and manure methane emissions for dairy cows prior to entering the milking herd and over a lactation period (i.e. whilst lactating and non-lactating) per kg of energy corrected milk (ECM), 2) identify the main factors influencing a dairy cow's total lifetime methane emissions per kg ECM and 3) suggest how animal and system effects could contribute to effective methane emission mitigation strategies. This study utilised production data to predict enteric and manure methane emissions from the Langhill herd to evaluate genetic line × feeding system interactions. The data were obtained from January 1990 to June 2008. Total methane emissions (i.e. enteric and manure) were estimated for 824 cows, for a total of 1,639 lactations. Total methane emissions from non-milking cows and manure methane emissions for lactating cows were predicted using Intergovernmental Panel on Climate Change (IPCC) Tier II methodology (1997), while enteric methane emissions for lactating cows were estimated using a non-linear equation (Mills *et al.*, 2003) based on metabolisable energy (ME) intake. Residual Maximum Likelihood was used to assess the effect of lactation number, genetic line, feeding system, as well as the main factors influencing dairy system methane emissions. Results show that cows maintained on the low forage feeding system produced about 8% less enteric methane emissions per kg ECM compared to the high forage system. At Farm 2, there was no difference in total methane emissions between a non-grazing low forage feeding system and a high forage system because lower enteric methane emissions were compensated for by higher

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manure methane emissions associated with slurry production. Cows selected for increased milk fat plus protein production (Select) had lower total methane emissions per kg ECM up to their third lactation but, over a lifetime, there appears to be no meaningful reduction compared to Control cows. Higher dry matter intake and a longer lactation period, which were positively correlated with average ECM yield, were associated with lower total lifetime methane emissions per kg ECM.

Key Words: Dairy cattle, methane, lactation period, lifetime, system.

4.2 Introduction

It is recognised that within dairy systems the largest source of methane emissions is from enteric fermentation. In contrast, about 16 to 22% of total system emissions are from manure, as reported by Hindrichsen *et al*. (2005) for a range of diets. Generally, dry matter (DM) intake and nutrient intake have been found to be suitable predictors of enteric methane output from dairy cows (Mills *et al.,* 2003; Ellis *et al.,* 2007; Bell *et al.,* 2009). In contrast, manure methane production is influenced mainly by its organic matter content (e.g. slurry versus solid manure) and climatic factors (Kebreab *et al.,* 2006a). Manure methane production can be estimated using IPCC (1997; 2006) methodology.

Improved productivity and efficiency of livestock production through animal breeding and nutrition is one of the most promising ways to reduce methane emissions (Steinfeld *et al.,* 2006). Increased production efficiencies of cattle generally come from improved feed utilisation (Hegarty, 2005; Eastridge, 2006; Kebreab *et al.,* 2006a) and optimisation of livestock numbers for the level of production (Garnsworthy, 2004; Kebreab *et al.,* 2006a; Tamminga *et al.,* 2007). Bauman *et al.* (1985) found that improvements in production efficiency of cows (i.e. the ratio of milk yield to resource input), are due to a dilution of maintenance energy requirements. High yielding dairy cows, with high feed intakes and high enteric methane outputs are associated with a lower enteric methane

output per kg milk as they partition more of their nutrient intake towards milk production (Chapter 3).

The objectives of this study were to: 1) assess effects of lactation number, genetic line and feeding system on estimates of enteric and manure methane emissions (per animal and per kg energy corrected milk [ECM]) using data from the Langhill genetic line × feeding system experiment, 2) identify the main factors influencing a dairy cow's total lifetime methane emissions per kg ECM and 3) suggest how animal and system effects could contribute to effective methane emission mitigation strategies.

4.3 Materials and Methods

4.3.1 Data

The data used were collected from January 1990 to June 2008 for lactating and non-lactating periods (referred to as the lactation period) of individual herd cows, as well as the period prior to the cow entering the milking herd. The data are described in Section 1.3.3. Prior to entering the milking herd, heifers were weighed each spring and autumn each year. The length of the lactation period was defined as from one calving to the next or to being culled from the herd. Milk yields were converted to energy corrected milk (ECM) yield (Sjaunja *et al.*, 1990):

$$\text{ECM (kg/day)} = 0.25 \times \text{kg milk yield} + 12.2 \times \text{kg milk fat} + 7.7 \times \text{kg milk protein}$$

4.3.2 Methane emission prediction

Total methane emissions from enteric fermentation and manure were estimated for each cow prior to entering the milking herd and whilst in the milking herd over a lactation. Methane emissions for cows prior to entering the milking herd were calculated from birth until they calved for the first time. The IPCC Tier II methodology (IPCC, 1997) was used to predict methane emissions from enteric fermentation and manure for the period prior to a cow entering the milking herd and whilst not lactating. To maintain

consistency in manure predictions, manure methane emissions for lactating cows were also predicted using the IPCC (1997) Tier II methodology. The following assumptions were fixed in the IPCC calculations, based on UK GHG inventory values being: digestibility of feed GE of 0.65; enteric methane conversion factor of 0.06 of GE intake; ash content of manure of 0.8; methane producing capacity of manure of 0.24 m^3/kg volatile solids; manure methane conversion factor of 0.1 for slurry and 0.01 for solid manure (UKGGI, 2008). Cows prior to entering the milking herd and cows non-lactating were assumed to be fed the same diet with the same digestibility, based on Tolkamp *et al.* (1998) who studied diets fed to Langhill herd cows where negligible differences in feed digestibility occurred. All cows were assumed to produce solid manure except for lactating cows indoors which produced slurry.

Enteric methane predictions for lactating cows was estimated using daily DM intake records when cows were indoors, and predicted pasture DM intakes when cows were grazing. When lactating cows were at pasture during the summer, pasture daily DM intake was predicted using the NRC (2001) model as:

$$\text{DM intake (kg/day)} = 0.372 \times [0.4 \times \text{kg milk yield} + 15 \times (\text{kg milk fat} / 100) \times \text{kg milk yield}] + [0.0968 \times \text{live weight}^{0.75}] \times 1 - e^{(-0.192 \times \text{week of lactation}) + 3.67}$$

The NRC (2001) DM intake prediction model was identified in Chapter 3 as suitable for predicting pasture intake for Langhill herd cows. Daily DM intake was then multiplied by the ME content of the food consumed to give daily ME intake. The following non-linear equation of Mills *et al.* (2003) was used to predict enteric methane output:

$$\text{Methane output (MJ/day)}^{-} = 45.98 - (45.98 + 0) \times e^{[-0.003 \times \text{ME intake}]}$$

This equation was identified in a previous study (Bell *et al.,* 2009, which has subsequently been updated as shown in Chapter 2) as suitable for the wide range of values seen in the Langhill herd data. Predicted daily enteric methane outputs were then

averaged to provide an estimate of emissions for the full lactation. In addition, enteric methane emissions of lactating cows were estimated using the IPCC Tier II methodology, based on 6% of GE intake being lost as methane, and the results were compared to those obtained using the Mills *et al.* (2003) equation. Methane emissions were expressed in kilograms and grams per kg ECM.

4.3.3 Effects of lactation number, genetic line and feeding system

Over the study period there were 1,639 lactation periods from 824 cows with estimates of total methane emissions both during the lactation phase and prior to entering the milking herd (Table 13). The 1,689 lactation periods were comprised of the 2 × 2 factorial genetic line × feeding system experiment at Farm 1 and 2

Table 13. Number of estimates of total methane emissions for lactations 1 to 3+, cumulative emission estimates for 3 lactations or less or over a lifetime for each genetic line × feeding system* at Farm 1 and 2

		Farm 1				Farm 2				
	No.	LFC	LFS	HFC	HFS	LFC	LFS	HFC	HFS	Total
Lactation	1	103	135	92	143	42	47	37	36	635
	2	64	96	74	84	33	29	32	32	444
	3	55	72	54	52	30	19	28	25	335
	3+	24	30	34	31	26	20	27	33	225
	Total	246	333	254	310	131	115	124	126	1,639
	Cows	123	155	113	159	69	72	70	63	824
3 lactations or less	Cows	43	51	36	48	15	24	8	15	240
Lifetime	Cows	24	20	26	27	10	19	2	11	139

* LFC = Low Forage Control, LFS = Low Forage Select, HFC = High Forage Control and HFS = High Forage Select.

Average values for DM and ME intakes, milk yield, milk fat and protein contents, and live weight of cows within each production system are in Table 14, from which methane predictions and estimates were calculated.

Table 14. Mean (s.e.) dry matter (DM) intake, metabolisable energy (ME) intake, daily energy corrected milk (ECM) yield, milk fat and protein contents and live weight for lactating cows in each genetic line × feeding system* at Farm 1 and 2

		Farm 1				Farm 2			
Trait		LFC	LFS	HFC	HFS	LFC	LFS	HFC	HFS
DM intake	kg/day	18.1	20.4	16.3	17.7	18.2	20.5	16.4	16.8
		(0.2)	(0.2)	(0.2)	(0.2)	(0.2)	(0.2)	(0.4)	(0.5)
ME intake	MJ/day	225	247	200	213	203	227	200	216
		(1.5)	(1.5)	(1.5)	(1.5)	(2.8)	(3.3)	(1.9)	(1.9)
ECM yield	kg/day	22.8	28.7	20.3	24.5	27.7	33.4	23.5	27.4
		(0.3)	(0.3)	(0.2)	(0.3)	(0.4)	(0.5)	(0.3)	(0.3)
Milk fat	g/kg	41.5	42.0	43.1	43.7	36.4	37.8	39.7	41.1
		(0.3)	(0.3)	(0.3)	(0.3)	(0.5)	(0.5)	(0.4)	(0.5)
Milk protein	g/kg	32.9	33.3	32.4	32.2	32.1	32.8	31.7	32.8
		(0.1)	(0.1)	(0.1)	(0.1)	(0.2)	(0.2)	(0.2)	(0.2)
Live weight	kg	598	609	590	586	640	649	616	637
		(4.4)	(3.0)	(4.0)	(3.2)	(6.0)	(6.2)	(5.9)	(5.2)

* LFC = Low Forage Control, LFS = Low Forage Select, HFC = High Forage Control and HFS = High Forage Select.

The data were analysed using Genstat Version 11.1 (Lawes Agricultural Trust, 2009) and Restricted Maximum Likelihood. Differences between estimated total enteric and manure methane emissions for fixed effects of lactation number, genetic line and feeding system were investigated where appropriate prior to heifers entering the milking herd and over a cow's lactation period per kg ECM. The linear mixed model used to assess differences in enteric and manure methane emissions, heifer growth rate, GE intake and days from birth to first calving was:

$$Y_{ijk} = \mu + L_i + G_j \times F_k + C_{ijk} + Yr_{ijk} + M_{ijk} + E_{ijk}$$

where, Y_{ijk} = total enteric and manure methane emissions prior to entering the milking herd (kg) and over a lactation period (g/kg ECM), heifer growth rate (kg/day), GE intake (MJ/day) and days from birth to first calving; μ = overall mean; L_i = fixed effect of lactation number (1, 2, 3 and 3+); G_k = fixed effect of genetic line (Control or Select); F_j

= fixed effect of feeding system (Low Forage or High Forage feeding system at Farm 1 and 2); C_{ijk} = random effect of cow; Yr_{ijk} = random effect of year of calving; M_{ijk} = random effect of month of calving; E_{ijk} = random error term.

Models for heifers prior to entering the milking herd did not include the fixed effect of lactation number (L_i). The profiles of estimated enteric and manure methane emissions per kg ECM were obtained as the interaction between genetic line and year of calving, as well as feeding system and year of calving. Significance was attributed at $P < 0.05$.

4.3.4 Influential factors associated with lifetime emissions

There were 240 cows with estimates of total methane emissions from birth to the end of their third lactation, or to when they were culled if earlier (Table 13). For 139 of these cows, there were also estimates of total methane emissions beyond their third lactation to the end of their milking life (i.e. lifetime emissions). The significant explanatory variables associated with methane emission estimates per kg ECM for a) lactation periods 1 to 3 or less if the cow was culled, or b) over a lifetime were compared. This was to test if the sample of 139 cows with a lifetime estimate of total methane emissions per kg ECM could be considered to be from the same population as the 240 cows with estimates up to their third lactation.

The information recorded and included in the lifetime analyses were: lactation number, genetic line, feeding system, live weight, length of non-lactating period, lactation length, calving interval, gestation length and health (i.e. unhealthy = 1, healthy = 0). The fertility measures recorded and included in the analyses were: days from calving to first service and from calving to conception, days from calving to first heat observed and number of services. The DM intake, ECM yield, milk composition and live weight were averaged over a lactation. Total ECM production per lactation and lifetime were also calculated. Continuous variables in the lifetime model were averaged over the cow's individual lactations. Additional variables included in the lifetime methane emissions analyses were age at first calving and age at last calving. Some of the explanatory

variables included in the analyses were input variables used in methane predictions, such as DM intake, milk yield, live weight, and milk fat and protein contents. However, the aim of the multivariate analysis for lifetime methane emissions was to incorporate sufficient additional variables to describe the dairy system effectively per kg ECM.

Effects of the explanatory variables (or factors) on total methane emissions per kg ECM per cow were evaluated for a) lactation periods 1 to 3 or less if the cow was culled or b) over a lifetime, and compared using a linear mixed model. Wald tests, which use χ^2 distribution, were used to assess the significance of factors. The continuous factors (i.e. the production and fertility traits mentioned above) were separated into four classes using interquartile ranges of each variable, thus preventing outlying data from confounding the results. Each factor was first analysed in a univariate analysis per cow. The most significant factors from the univariate analysis were added first to a multivariate model with only significant variables being retained. The proportion of phenotypic variation associated with each influential factor was determined.

A linear mixed model was also used to assess the difference in total methane emissions per kg ECM for genetic line × feeding system for a) lactation periods 1 to 3 or less if the cow was culled, or b) over a lifetime. Spearman's rank correlation was used to test the association between total estimated methane enteric emissions for lactating cows using the non-linear Mills *et al.* (2003) equation and the IPCC (1997) Tier II methodology. Pearson correlation coefficient was used to test the association between influential factors and average ECM yield. Significance was attributed at $P < 0.05$.

4.4 Results

4.4.1 Milking herd and herd replacement methane emissions

The average number of lactations per cow during the study period was 2.2 ± 0.03 (median of 2), with a culling rate within the herd of 0.25 ± 0.02 per year. Prior to entering the milking herd, milking herd replacements averaged 751 ± 2.9 d from birth to

first calving with an average live weight of 295 ± 1.3 kg. Once in the milking herd, lactating cows averaged 7,686 ± 62 kg ECM per cow for an average lactation of 322 ± 1.9 d and non-lactating period of 58.8 ± 0.5 d where cows averaged 655 ± 2.1 kg live weight at the time of drying off.

Total predicted enteric methane emissions whilst cows were lactating using the non-linear equation of Mills *et al. (*2003) showed a high and positive rank correlation (r = 0.89, $P < 0.001$) when compared to emissions calculated using the IPCC (1997) Tier II methodology, suggesting that using either method would give comparable results over a lactation. Total enteric methane emissions for a cow whilst lactating using the non-linear equation of Mills *et al.* (2003) were 128 ± 0.8 kg and using the IPCC (1997) Tier II methodology 132 ± 0.8 kg. Within the milking herd, total enteric methane emissions accounted for 85% of total methane emissions over a lactation period (i.e. 137 ± 0.8 kg from enteric methane and 25 ± 0.2 kg from manure methane emissions).

4.4.2 Effect of lactation number, genetic line and feeding system

Differences between production systems at Farm 1 and 2 are in Table 15. Prior to entering the milking herd, replacement cows from the Select genetic line had higher total methane estimates from their enteric fermentation and manure ($P < 0.001$). The difference in total methane emissions prior to entering the milking herd was because Select heifers had a higher GE intake of 139 MJ/day compared to 130 MJ/day for Control heifers (SED = 1.2, $P < 0.001$). The higher GE intake of Select heifers was required to meet their growth rate of 0.68 kg/day compared to 0.64 kg/day for Control cows (SED = 0.01, $P < 0.001$). There was no difference in the number of days from birth to first calving between genetic lines.

Table 15. Predicted means for total enteric (EF) and manure methane estimates for cows prior to entering the milk herd and over a lactation period per kg energy corrected milk (ECM) for different lactations, genetic lines and feeding systems

		Prior to entering milking herd		Lactation Period		
Fixed effect		EF kg	Manure kg	EF g/kg ECM	Manure g/kg ECM	EF + Manure g/kg ECM
Lactation number	1			18.3	3.2	21.6
	2	-	-	17.0	3.0	20.0
	3	-	-	16.5	3.0	19.5
	3+	-	-	16.0	3.0	19.0
	SED	-	-	0.21***	0.03***	0.22***
Genetic line	Control	105.9	2.8	18.3	3.2	21.5
	Select	114.6	3.0	15.6	2.9	18.5
	SED	1.5***	0.04***	0.29***	0.04***	0.31***
Feeding system	LF Farm 1	107.5	2.8	17.4	2.9	20.4
	HF Farm 1	106.4	2.8	18.1	3.2	21.3
	LF Farm 2	110.9	2.9	15.2	4.0	19.2
	HF Farm 2	116.4	3.0	17.4	2.1	19.2
	SED	3.0	0.08	0.50***	0.08***	0.53***

LF = Low Forage, HF = High Forage; SED = standard error of the difference between means; *** $P < 0.001$.

Once in the milking herd, Table 15 shows that, compared to first lactation cows, older cows had lower estimated enteric and lower manure methane emissions per kg ECM (both $P < 0.001$) for a total of 12% lower emissions. Also, compared to Control genetic line cows, Select cows had lower estimated enteric and lower manure methane emissions per kg ECM (both $P < 0.001$), which lowered total emissions by about 14%. Fig. 7 shows that over the study that enteric methane emissions per kg ECM for both genetic lines had a declining trend over time. In terms of feeding system, non-grazing cows at Farm 2 on a Low Forage diet had the lowest estimated enteric methane emissions per kg ECM (about 13% lower than the High Forage feeding system at Farm 2), but these cows had the highest manure emissions per kg ECM (both $P < 0.001$; Table 15). A Low Forage feeding system, whether at Farm 1 or 2, had 8% lower enteric methane emissions per kg ECM than a High Forage feeding system. The High Forage feeding system at Farm 2 had the lowest estimated manure emissions per kg ECM (about 28% lower than

the next lowest feeding system ($P < 0.001$; Table 15 and Fig. 7). However, overall, non-grazing Low Forage and High Forage feeding systems at Farm 2 both had the lowest total methane emissions per kg ECM over a lactation period (Table 15, both 19.2 g/kg ECM; $P < 0.001$). There was no interaction between genetic line and feeding system.

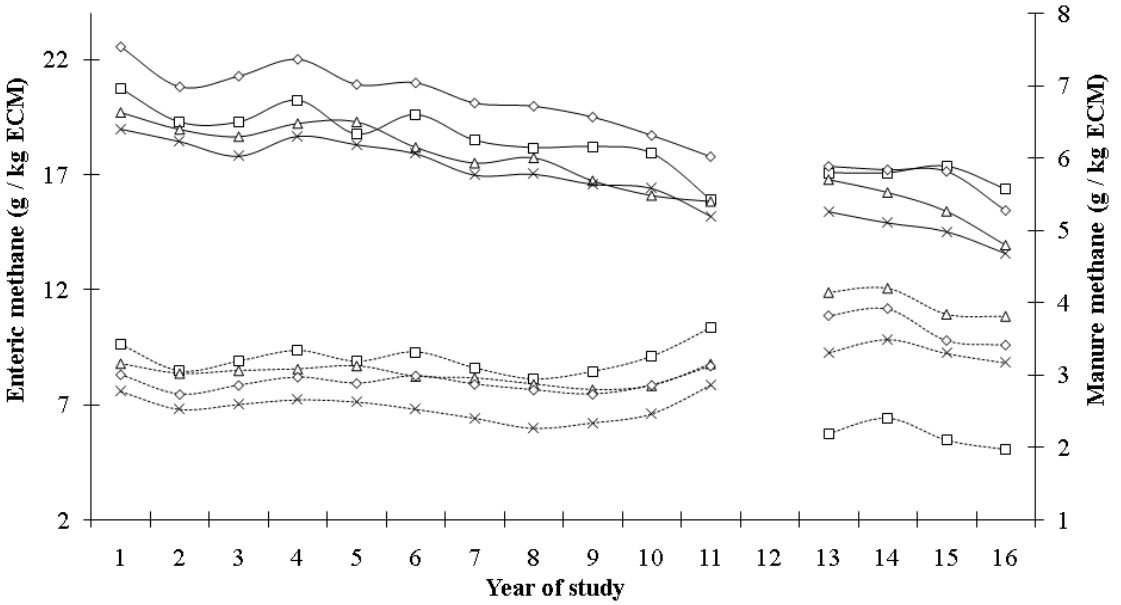

Fig. 7. Predicted mean estimated methane emissions per kg energy corrected milk (ECM) (— enteric and --- manure methane) for Control (◊) and Select (×) genetic lines as well as for High Forage (□) and Low Forage (Δ) feeding systems during the study period. Year 12 was when cows moved from Farm 1 to Farm 2.

4.4.3 Influential factors affecting lifetime emissions

There were 139 cows in the dataset that had lifetime methane emission estimates (Table 13) beyond their third lactation. Of the total lifetime methane emissions produced by a cow, on average 29% were produced prior to entering the milking herd (391 ± 13.9 kg of which 113 ± 1.4 kg were prior to entering the milking herd). The average number of lactations for cows with complete lifetime emissions was 1.86 ± 0.08 per cow. The significant factors for a cow's complete lifetime were also the significant factors for the

subset of 240 cows (Table 13) that had lifetime methane emissions up to their third lactation or less. Table 16 shows that the main factors describing estimated methane emissions per cow per lifetime were lactation period length and DM intake.

Table 16. Results from the multivariate analysis showing the main influential factors associated with a cow's complete lifetime methane emissions g/kg energy corrected milk (ECM)

Factor		Methane g/kg ECM	Wald statistic	df	SED	*P value*	% of phenotypic variation
Lactation period length (d)	<281	70.2	44.5	3	6.9	<0.001	0.75
	281 to 341	34.7					
	342 to 379	30.9					
	>379	31.3					
Dry matter intake (kg/day)	<13.8	55.4	15.1	3	6.9	<0.01	0.25
	13.8 to 16.3	45.8					
	16.4 to 18.4	34.5					
	>18.4	31.4					

SED = standard error of the difference.

The largest proportion (0.75) of phenotypic variation associated with lifetime methane emissions was associated with lactation period length rather than daily DM intake (0.25). Unexplained variation was negligible. Average ECM yield over a cow's lifetime was positively correlated with lactation period length ($r = 0.25$, $P < 0.01$) and DM intake ($r = 0.60$, $P < 0.001$). However, Select genetic line cows did not have a different estimate for their total methane emissions per kg ECM compared to Control animals over a complete lifetime. Select and Control genetic line cows had significantly different estimated total methane emissions per kg ECM up to their third lactation or less per kg ECM (32.1 and 40.9 g/kg ECM respectively; SED = 4.8, $P < 0.05$). There was no difference between feeding systems in total methane emissions per kg ECM per cow up to their third lactation or less and over a cow's lifetime.

4.5 Discussion and conclusions

Results suggest that cows selected for increased milk fat plus protein production (i.e. Select genetic line cows) have lower total methane emissions per kg ECM up to their third lactation. A study by van de Haar and St. Pierre (2006) found that maximum lifetime energy efficiency is typically reached after three lactations, when mature size

and maximum milk production are achieved. These authors suggested that when maximum energetic efficiency is reached, environmental waste such as energy lost as enteric or manure methane will be minimised. In the present study, an increase in lactation number was associated with a reduction in estimated enteric and manure methane emissions per kg ECM. However, by maintaining older, more efficient cows within the dairy system, genetic progress will be slowed, though in practice modern Holstein-Friesian dairy cows are associated with poor health and fertility (Pryce *et al.*, 1999). Therefore, the incidence of involuntary culling (due to poor health and fertility) is relatively high in Holstein-Friesian dairy systems, which increases the system emissions associated with retaining milking herd replacements (Garnsworthy, 2004). But culled cow meat may well be used in the human food chain, substituting the emissions associated with other edible meat sources such as those from beef production. During the study, the culling rate of the milking herd was approximately 25% per annum, which is within the range of 25 to 30% suggested by Bascom and Young (1998) as being the optimum for farm profitability. The number of replacements needed influences the productivity and profitability of the herd. At a high rate, replacement costs are high but at too low a rate the milk production, reproduction or genetic improvement of the herd may be impaired (Hadley *et al.,* 2006). Future work could develop a whole system model to assess the optimum system in terms of profitability, productivity (including genetic improvement) and environmental impact.

By having a high genetic potential to mobilise body energy reserves for production, Coffey *et al.* (2006) found that heifers selected for increased milk fat plus protein prduction grew faster prior to entering the milking herd than Control line heifers. Thus, mature size was reached sooner for Select heifers than for Control heifers (Coffey *et al.*, 2006). However, heifers from the Select line did not enter the milking herd sooner, as it was management practice to bring replacement animals into the milking herd at about 2 years of age. A faster growth rate means that less energy is used for maintenance from birth to first calving, which leads to increased energetic efficiency and reduced methane losses per unit live weight gain (van de Haar and St Pierre, 2006). Changes in energy

efficiency of heifers can have substantial impact given that on average 29% of the total lifetime methane emissions comes from the period prior to cows entering the milking herd. If more of the animal's nutrient intake is partitioned towards production, as described by Bauman et al. (1985), a dilution of required energy for maintenance occurs. As a result of high energetic efficiency up to their mature size and maximum milk production (van de Haar and St Pierre, 2006). Select genetic line cows in this study had a lower estimated methane output per unit product during early life but not over a lifetime compared to Control genetic line cows. A high genetic potential for mobilising body energy reserves for production can have a deleterious effect on health and fertility, as Pryce *et al.* (1999) found with the Select genetic line cows in the Langhill herd. Maintaining healthy and fertile cows can offer savings in methane emissions per unit product as a result of more efficient production (Garnsworthy, 2004), particularly later in life as suggested by Wall *et al.* (2010a) and over the lifetime of Select genetic line animals as shown in our study. However, higher average daily DM intake and a longer lactation period, which is increased by poor fertility, which are positively correlated with average ECM yield are associated with lower estimated total lifetime methane emissions per kg ECM. Therefore, maintaining milk productivity in terms of average yield per cow can help minimise dairy system methane emissions per unit product.

Over the period of the study, there was a declining trend in estimated enteric methane emissions per kg ECM. The results in Chapter 3 showed that selection for kilograms of milk fat plus protein production in both genetic lines produced large reductions in enteric methane per kg milk of 19% and 23% for Select and Control genetic lines respectively. The enteric methane predictions for lactating cows in this study and in Chapter 3 utilised extensive dietary information based on a previous study (Bell *et al.*, 2009) that indentified the non-linear Mills et al. (2003) prediction equation using ME intake as suitable for the Langhill data. However, use of the IPCC methodology predicted enteric methane emissions from lactating cows reasonably similar to the Mills *et al.* (2003) equation, with a rank correlation of 0.89. Thus, the IPCC methodology estimate for enteric emissions would have been useful had DM intake records not been

available. By not using DM intake records to model enteric methane output, the results from Chapter 3 showed that methods to predict enteric methane output by modelling the energy requirements of a cow (i.e. IPCC Tier II method) over-predicted enteric methane output during the first 11 weeks of a lactation, hence a reason to use the available daily DM intake records in this study.

Changes in management of the herd from Farm 1 to 2 appear to have brought changes in estimated methane emissions for different feeding systems. It is a limitation of this study that manure methane emission estimates are based on fixed assumptions. Also, there was assumed to be no dietary effect on feed digestibility when feeding high quality diets, based on findings of Tolkamp *et al.* (1998) who studied Langhill herd diets. Manure emissions contributed only 15% of the total emissions during the lactation period, which is slightly lower than the 16 to 22% reported by Hindrichsen *et al.* (2005) for a range of diets. As a result of differences in manure methane production in our study, there was no difference in total methane emissions per kg ECM between the non-grazing Low Forage feeding system and the High Forage feeding system at Farm 2. Even though the non-grazing Low Forage feeding system was associated with lower enteric methane emissions per kg ECM by about 13% compared to the High Forage system at the same farm, the reduction was partially offset by the higher manure emissions associated with slurry production. Cows at Farm 2 on a High Forage feeding system had the lowest estimated manure methane emissions per kg ECM of the feeding systems studied. A difference in calving patterns between Farm 1 and 2 appears to have had an effect on dairy system emissions. Cows at Farm 1 on a High Forage system calved from September to January compared to all year round calving at Farm 2. As a result, Farm 1 cows were indoors at the peak of their milk production, and were producing slurry with a higher assumed methane producing potential than the solid manure typically produced at pasture. Cows at Farm 1 would be towards the end of their lactation period during the summer when at pasture, whereas at Farm 2 productivity is spread more evenly over the year with cows calving throughout the year. The housed

environment could however allow use of technology such as an anaerobic digester to capture methane emissions to generate electricity (Cantrell *et al.*, 2008).

In conclusion, this study suggests that a non-grazing low forage feeding system result in the lowest enteric methane emissions per kg ECM, with about 13% less enteric methane compared to a high forage feeding system at the same farm. However, the higher manure emissions associated with slurry production partially offset the reduction in enteric methane when compared to a feeding system that utilises pasture. Select genetic line cows were associated with lower estimated total methane emissions per kg ECM up to their third lactation, but not over a lifetime compared to Control genetic line cows. However, higher average DM intake and a longer lactation period, both of which were positively correlated with average ECM yield, were associated with lower lifetime methane emissions per kg ECM. The next Chapter includes the other important emissions from dairy systems, which are nitrous oxides and carbon dioxide, in order to assess the effect of changing production parameters on whole farm GHG emissions.

Chapter 5 The effect of improving cow productivity, fertility and longevity on the global warming potential of dairy systems

5.1 Summary

This study compares the environmental impact of a range of dairy production systems in terms of their global warming potential (GWP, expressed as carbon dioxide equivalent [CO_2-eq.] emissions) and associated land use, and explores efficacy of reducing said impact. A Markov chain approach was used to describe the production systems within the Langhill herd between October 2003 and October 2008, to help estimate the CO_2-eq. emissions per year and land required per cow. A partial life cycle assessment (LCA) was used to estimate the CO_2-eq. emissions and land use of each production system and the herd average. The CO_2-eq. emissions were expressed per kg energy corrected milk (ECM) and per hectare of land use, as well as land required per kg ECM. The effect of a phenotypic and genetic standard deviation unit improvement in herd feed utilisation efficiency, ECM yield, calving interval length and incidence of involuntary culling were assessed. Results show that a low forage (non-grazing) feeding system with Select cows produced the lowest CO_2-eq. emissions of 1.1 kg/kg ECM and land use of 0.65 m^2/kg ECM but the highest CO_2-eq. emissions of 16.1 t/ha of the production systems studied. Within the herd, a standard deviation improvement in feed utilisation efficiency was the only trait of those studied that would significantly reduce the reliance of the farming system on bought-in synthetic fertiliser and concentrate feed, as well as reduce the average CO_2-eq. emissions and land use of the herd (both by about 6.5% of which about 4% would be achievable through selective breeding). Within production systems, reductions in CO_2-eq. emissions per kg ECM and CO_2-eq. emissions per hectare are also achievable by an improvement in feed utilisation. This study has developed models that harness the biological trait variation in the animal to improve the environmental impact of the farming system. Results show that genetic selection for efficient feed use for milk production according to their feeding system can bring about reductions in system nutrient requirements, CO_2-eq. emissions and land use per unit product.

Key Words: Dairy cow, production system, Markov chain, global warming potential, land use.

5.2 Introduction

Capper *et al.* (2009) highlighted the need to adopt management practices and technologies that improve productive efficiency to meet increasing product demand (FAO, 2010) while minimising the environmental impact of dairy production. The environmental impact of a system can be evaluated by assessing the GWP in carbon dioxide equivalent (CO_2-eq.) emissions and resource use (in the context of this paper, land use) associated with production (Guinée *et al.*, 2002). The land use associated with a dairy system reflects the cow's requirement for food. The life cycle assessment (LCA) of a product has become an internationally accepted method for assessing its potential environmental impact (Guinée *et al.*, 2002). Several studies (Cederberg and Mattsson, 2000; Casey and Holden, 2005; Thomassen *et al.*, 2008; Basset-Mens *et al.*, 2009; FAO, 2010) have assessed the CO_2-eq. emissions of producing '1 kg of energy corrected milk (ECM) leaving the farm-gate' (the functional unit as defined by Guinée *et al.*, 2002) for a range of dairy production systems using national data. The use of ECM was first proposed by Sjaunja *et al.* (1990) to adjust milk yield for its fat and protein contents, which significantly affects the energy required to produce milk.

Globally, the dairy sector contributes about 4% of CO_2-eq. greenhouse gas (GHG) emissions (FAO, 2010). Carbon dioxide, methane, nitrous oxide as well as indirect sources of nitrogen from nitrogen oxides (NO_x) and ammonia (NH_3) contribute to the CO_2-eq. emissions of a production system. In developed countries 52% of dairy sector CO_2-eq. emissions are estimated to be in the form of methane, 27% nitrous oxide and 21% carbon dioxide (FAO, 2010). Methane from enteric fermentation is recognised to be the most important GHG from ruminant production systems, representing a significant loss of between 2% to 12% of gross energy (GE) intake (Martin *et al.*, 2010). Nutritional manipulation of the diet is a mitigation option that can be applied

immediately through adjustments to management (Martin *et al.*, 2010), whereas selective breeding on a production trait such as feed utilisation efficiency would take several years before any genetic improvement is seen (Hegarty, 2005).

Garnsworthy (2004) found that a high milk producing system with a high health and fertility status offers scope for minimising methane emissions per kilogram of milk by reducing the number of milking herd replacements retained and the calving interval length, and increasing the average daily milk yield of the herd. However, as a result of breeding largely for increased milk production in Holstein-Friesian dairy cows over the last twenty five years, there has been an associated reduction in genetic merit for fitness traits such as health and fertility (Pryce *et al.*, 1999). Garnsworthy (2004) modelled fertility parameters and found that the emissions of methane have risen by 11% per herd compared to 1995 fertility levels in the UK. Results from the study in Appendix A showed that poor fertility (longer days from calving to conception and conception failure) and poor health (calving assistance, abortion and mastitis) were risk factors to survival of cows in the Langhill herd.

Wall *et al.* (2010a) highlighted the need for work to assess the role that genetic improvement can have in a whole system approach to GHG emissions, including its interaction with feeding and management systems. The production systems in this study were designed to represent average and high genetic lines for production on low (non-grazed) or high forage (with grazing) feeding systems (Pollott and Coffey, 2008), but in contrast to other studies were within the same farming unit thus minimising the impact of extraneous factors. Dairy systems can range considerably in their level of production and efficiency with regard to feed intake, milk yield, fertility and health, all of which can influence survival, CO_2-eq. emissions and the requirement for land. To model dairy systems within the same herd and farming unit on a comparative time frame, whilst incorporating the cyclical nature of individual systems and the implications of changes to these systems, a Markov chain (Agrawal and Heady, 1972) can be used. A Markov chain approach has been used to model the effects of production factors such as disease

(Allore and Erb, 1999) and fertility (Stott *et al.*, 1999; Garnsworthy, 2004) on a herd. Stott *et al.* (1999) used a Markov chain to establish the economic optimum total cost of fertility in a dairy herd. Santarossa *et al.* (2004) incorporated this approach in an assessment of the sustainability of dairying.

The objectives of the present study were to: 1) model the CO_2-eq. emissions and land use of the Langhill experimental herd using a Markov chain and LCA approach, 2) assess for each production system within the herd the effect of a phenotypic and genetic standard deviation improvement in herd feed utilisation efficiency, ECM yield, calving interval length and involuntary culling on the CO_2-eq. emissions and land use of the herd, 3) assess the effect of the same improvements on CO_2-eq. emissions and land use per kg ECM and CO_2-eq. emissions per hectare, and 4) suggest feasible mitigation options.

5.3 Materials and Methods

5.3.1 Production systems

The data used in this study were collected from October 2003 to October 2008. The data are described in Section 1.3.3. During the study period, the Low Forage diet consisted on average of 50% home-grown forage (grass silage, maize silage and ammonia treated wheat silage) and the High Forage diet was on average 75% home-grown forage in the DM, with High Forage cows on average having access to pasture for 55% of the days in a year (typically indoors November to April). The remaining proportion of the diet was bought-in concentrate feed in the form of wheat grain, sugar beet pulp, soyabean meal, rapeseed meal, wheat and barley distillers' dark grains, and vitamin and mineral supplement. Pasture DM intake was estimated using the NRC (2001) intake prediction model, which was shown in Chapter 3 to be an appropriate method for this study. Pasture GE was assumed to be 18.45 MJ/kg for nitrogen excretion calculations (UKGGI, 2008). The average percentage of dietary components in the DM of feed consumed during the study period for Low and High Forage milking herd diets respectively were:

grass silage 31.2% and 24.0%, maize silage 9.4% and 8.2%, ammonia treated wheat silage 9.4% and 8.6%, bought-in concentrate feed 50.0% and 23.8%, pasture 0 and 35.4%, and negligible mineral supplement. Herd replacements were assumed to eat 100% pasture as information on their diet was not available.

Following Sjaunja *et al.* (1990) milk yields were converted to energy corrected milk (ECM):

$$\text{ECM (kg/day)} = 0.25 \times \text{kg milk yield} + 12.2 \times \text{kg milk fat} + 7.7 \times \text{kg milk protein}$$

Culling time was defined as the date on which a cow's productive life ceased. The reasons for culling cows prior to their fourth lactation were normally poor fertility, abortion or mastitis (Appendix A).

5.3.2 Markov chain

A Markov chain can be used to represent a herd as a vector of states (s) that cows occupy at a given point in time (Stott *et al.,* 1999). These states may represent lactation number, stage of lactation, disease status or pregnancy status etc. depending upon the objectives of the study. The vector of states at time t is multiplied by a matrix of transition probabilities (s×s) to give the vector of states at time t+1. If the transition matrix is constant for all stages i.e. the model is stationary, then repeated matrix multiplication will produce a fixed long-run (steady state) vector, which is independent of the initial state vector. This long-run steady state vector provides a useful basis for comparative assessment of the alternative dairy systems. Modelling the herd structure using a Markov chain also allowed changes in dairy system parameters to be systematically assessed at the herd level. Previous studies on the Langhill herd have typically modelled the production systems (genetic line × feeding system) within the herd using daily average values (Chagunda *et al.*, 2009).

To model the herd structure over time with a Markov chain we used a stage interval of 60 days was used. A maximum calving interval of 600 days covering all cows was assumed for lactations 1, 2, 3 and 3+, so the state vector consisted of 10 within calving interval periods of 60 days for each of four lactations (40 states in total). The proportion of the milking herd falling within each state depended on when cows calved or whether they were culled from the herd. Once cows calved they would move on to the next lactation unless culled from the herd. The percentage of cows calved and culled during each state for each lactation and production system is shown in Table 17. These data were used to construct a transition matrix for a Markov chain for each production system. The percentages calved and culled were converted into a transition probability from lactation n to n+1 and from lactation 1 to lactation n respectively. Cows culled were therefore assumed to be replaced within one stage interval, reflecting experimental practice whereby treatment group sizes are maintained within the herd. The data in Table 17 were accumulated over seven years and thus give the best available estimate of the calving and culling performance of each system under the conditions operating on the Langhill herd at this time, described in Section 1.3.3. The herd calving and culling data as incorporated into the Markov chain are therefore performance characteristics of the cows in each production system and exclude 'voluntary' culling for reasons dictated by the requirements of the herd manager as would be found in commercial herd data.

Table 17. Percentage of cows across states, lactations and production systems* studied that calved or were culled (from farm data) and the long-run steady state vector obtained from the Markov chain

Lactation no.	State	Calved (%)				Culled (%)				Steady state (%)			
		LFC	LFS	HFC	HFS	LFC	LFS	HFC	HFS	LFC	LFS	HFC	HFS
1	1	0.0	0.0	0.0	0.0	0.0	0.0	8.0	2.4	4.8	4.7	5.1	4.4
1	2	0.0	0.0	0.0	0.0	0.0	1.5	0.0	4.9	4.8	4.7	4.7	4.3
1	3	0.0	0.0	0.0	0.0	4.7	6.2	4.0	0.0	4.8	4.6	4.7	4.1
1	4	0.0	0.0	0.0	0.0	2.3	3.1	4.0	0.0	4.6	4.3	4.5	4.1
1	5	2.2	1.3	1.3	1.4	2.3	6.2	4.0	4.9	4.5	4.2	4.4	4.1
1	6	29.0	30.0	29.5	25.0	4.7	4.6	8.0	4.9	4.3	3.9	4.1	3.9
1	7	47.3	32.5	42.3	36.1	2.3	0.0	0.0	2.4	2.8	2.5	2.6	2.7
1	8	12.9	22.5	19.2	19.4	0.0	3.1	0.0	2.4	1.4	1.7	1.5	1.7
1	9	5.4	8.8	5.1	5.6	2.3	0.0	8.0	0.0	1.2	1.3	1.2	1.3
1	10	3.2	5.0	2.6	12.5	0.0	4.6	0.0	0.0	1.2	1.2	1.0	1.2
2	1	0.0	0.0	0.0	0.0	7.0	0.0	4.0	2.4	4.1	3.7	3.8	3.6
2	2	0.0	0.0	0.0	0.0	2.3	1.5	0.0	2.4	3.8	3.7	3.6	3.5
2	3	0.0	0.0	0.0	0.0	0.0	4.6	8.0	0.0	3.7	3.6	3.6	3.5
2	4	0.0	0.0	1.5	2.1	4.7	4.6	0.0	4.9	3.7	3.4	3.3	3.5
2	5	1.8	3.9	0.0	0.0	0.0	3.1	0.0	0.0	3.5	3.3	3.3	3.3
2	6	25.0	31.4	18.2	25.0	9.3	3.1	8.0	0.0	3.5	3.0	3.3	3.2
2	7	44.6	45.1	50.0	33.3	2.3	3.1	4.0	2.4	2.3	2.0	2.4	2.4
2	8	21.4	15.7	19.7	22.9	0.0	1.5	0.0	0.0	1.2	1.0	1.1	1.5
2	9	3.6	0.0	9.1	14.6	0.0	0.0	0.0	2.4	1.0	0.9	0.9	1.2
2	10	3.6	3.9	1.5	2.1	0.0	1.5	4.0	2.4	0.9	0.9	0.8	1.0
3	1	0.0	0.0	0.0	0.0	0.0	0.0	8.0	0.0	3.2	3.0	2.9	3.2
3	2	0.0	0.0	0.0	0.0	0.0	1.5	0.0	0.0	3.2	3.0	2.7	3.2
3	3	0.0	0.0	0.0	0.0	2.3	4.6	0.0	2.4	3.2	2.9	2.7	3.2
3	4	0.0	0.0	0.0	0.0	7.0	4.6	0.0	2.4	3.1	2.8	2.7	3.1
3	5	0.0	0.0	0.0	2.3	2.3	3.1	4.0	2.4	2.9	2.7	2.7	3.0
3	6	29.5	24.1	25.0	25.6	4.7	0.0	0.0	0.0	2.8	2.6	2.6	2.9
3	7	31.8	27.6	41.1	44.2	4.7	3.1	0.0	2.4	1.8	2.0	1.9	2.1
3	8	27.3	17.2	17.9	16.3	2.3	3.1	4.0	0.0	1.2	1.4	1.1	1.1
3	9	11.4	20.7	12.5	9.3	0.0	1.5	0.0	0.0	0.8	1.1	0.9	1.0
3	10	0.0	10.3	3.6	2.3	0.0	0.0	0.0	4.9	0.7	0.8	0.8	0.9
3 +	1	0.0	0.0	0.0	0.0	9.3	4.6	4.0	4.9	2.6	2.5	2.5	2.9
3 +	2	0.0	0.0	0.0	0.0	2.3	4.6	0.0	14.6	2.3	2.4	2.4	2.7
3 +	3	0.0	0.0	0.0	0.0	7.0	4.6	0.0	4.9	2.3	2.3	2.4	2.3
3 +	4	0.0	0.0	0.0	2.2	7.0	3.1	0.0	2.4	2.1	2.1	2.4	2.2
3 +	5	0.0	0.0	0.0	0.0	4.7	0.0	0.0	14.6	2.0	2.1	2.4	2.1
3 +	6	25.9	27.8	22.0	17.8	2.3	4.6	12.0	0.0	1.9	2.1	2.4	1.8
3 +	7	40.7	50.0	36.6	48.9	0.0	3.1	4.0	2.4	1.8	2.0	2.1	1.8
3 +	8	14.8	16.7	19.5	20.0	0.0	1.5	0.0	0.0	0.0	1.9	2.1	1.8
3 +	9	18.5	5.6	17.1	8.9	0.0	0.0	0.0	0.0	0.0	1.9	0.0	0.0
3 +	10	0.0	0.0	4.9	2.2	0.0	0.0	0.0	2.4	0.0	0.0	0.0	0.0

* LFC = Low Forage Control, LFS = Low Forage Select, HFC = High Forage Control and HFS = High Forage Select.

5.3.3 Life cycle assessment

Resource inputs required for the production of raw milk to the farm-gate, described below, were allocated to each production system based on the herd structure reflected in the Markov chain long-run (steady) state vector. A partial LCA was carried out to describe CO_2-eq. emissions and land use (on-farm and for bought-in feed) associated with each production system over a year. The impact from the production of agri-chemicals, seed, lime (and its application) and capital items were not included because these resources were either of low impact or did not vary with production system within the farm. Such simplifying assumptions were also made, by Cederberg and Mattsson, (2000) and Thomassen *et al.* (2008) for seed and capital items. The functional unit as defined by Guinée *et al.* (2002) was '1 kg ECM leaving the farm-gate'. To maintain consistency with other dairy system studies the GWP in CO_2-eq. emissions were calculated using conversion factors from methane and nitrous oxide to CO_2-eq. emissions of 21 and 310 (for a 100 year time horizon) respectively, which were expressed per kg ECM and per hectare (Cederberg and Mattsson, 2000; Casey and Holden, 2005; Thomassen *et al.*, 2008, Basset-Mens *et al.*, 2009). The sources of CO_2-eq. emissions were from enteric fermentation, manure and soils (from leaching, runoff, atmospheric deposition of nitrogen from nitrogen oxides and ammonia, and biological fixation of nitrogen), on-farm energy use (electricity and fuel), bought-in synthetic fertiliser and concentrate feed (Fig. 8).

5.3.4 Carbon dioxide equivalent emissions and land use

Emissions of methane, nitrous oxide and carbon dioxide were determined as well as the total land area required to meet the animals' feed requirements. Methane production included both enteric fermentation and emissions from manure. Enteric fermentation emissions were estimated from DM intake and GE intake using an equation of Mills *et al.* (2009). This equation was identified in Chapter 2 as suitable for the wide range of values seen in the Langhill herd data. The Intergovernmental Panel on Climate Change (IPCC) Tier II methodology (1997) was used to predict daily GE intake, with the IPCC

(2006) Tier II methodology then being used to determine manure methane and nitrous oxide emissions (from nitrogen excretion).

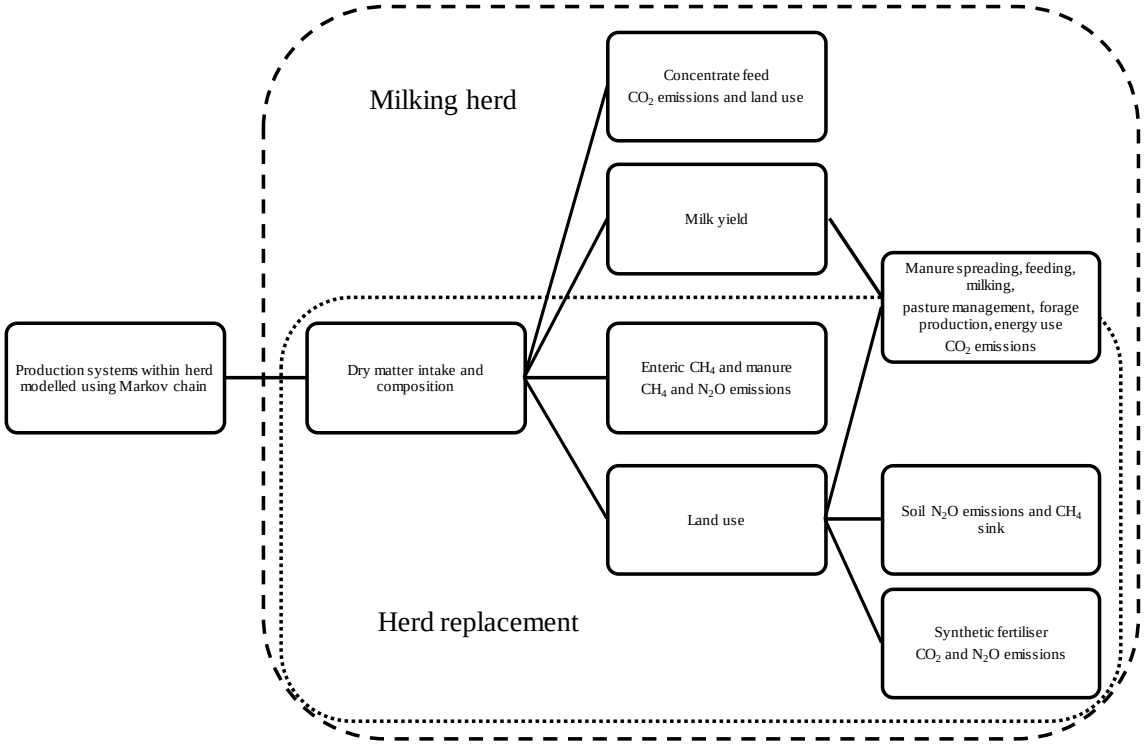

Fig. 8. Sources of methane (CH_4), nitrous oxide (N_2O) and carbon dioxide (CO_2) emissions from the milking herd (– –) and their replacement (···) modelled using a Markov chain and partial life cycle assessment.

The assumptions made in the IPCC calculations are shown in Table 18. Forage crops were assumed to leave no residues on the land. The average daily DM intake of a milking herd replacement was set at 6.83 and 7.15 kg/day for Control and Select genetic line animals respectively (obtained from data in Chapter 4). Both genetic lines were fed the same diet until they entered the milking herd. The DM intakes for Control and Select milking herd replacements were calculated using an IPCC (2006) Tier II methodology prediction equation, where estimates of DM intake were based on a dietary net energy concentration of the diet of 7.5 MJ/kg DM and average live weight of the

animal. The average live weight of Control and Select genetic line animals from birth to first calving were 285 ± 24 and 303 ± 26 kg respectively. Results from Chapter 4 showed that there was no difference in the number of days from birth to first calving between genetic lines, but Select genetic line animals had a higher growth rate and GE intake. Following Steinfeld *et al.* (2006), the amount of respired carbon dioxide was assumed to be the same as the net photosynthesis of the consumed plant matter. Thus the carbon dioxide emissions are those associated with supplying fertiliser, electricity and fuel to the farm and those emitted from fuel use (Table 18), as well as those from bought-in concentrate.

Table 18. Emission factors used to calculate methane (CH_4), nitrous oxide (N_2O) and carbon dioxide (CO_2) emissions associated with the production of raw milk

Gas/source	Equation/emission factor
Methane sources	
Enteric fermentation*	Methane (MJ/day) = [7.16 − (0.101 × DMI)] / 100 × GEI
Manure conversion factor†	1% at pasture and 10% indoors
Soil oxidation‡	2.5 kg ha^{-1} yr^{-1} for pasture and 1.5 kg ha^{-1} yr^{-1} for arable land
Nitrous oxide†	
Slurry	0.001 kg N_2O kg N^{-1}
Solid manure	0.02 kg N_2O kg N^{-1}
Direct soil emissions	0.0125 kg N_2O kg N^{-1}
Leaching and runoff	0.025 kg N_2O kg N^{-1}
Atmospheric deposition of nitrogen	0.01 kg N_2O kg N^{-1}
Grassland fixation	4 kg N^{-1} ha^{-1} yr^{-1}
Carbon dioxide§	
Synthetic fertiliser	6.847 kg CO_2-eq. kg N^{-1}
Electricity	0.042 kg CO_2-eq. L^{-1} milk
Fuel	3.8862 kg CO_2-eq. L^{-1}

* Mills *et al.* (2009), † UKGGI (2008), ‡ Boeckx and van Cleemput (2001), § Lovett *et al.* (2006). There were 1.03 kg L^{-1} milk. DMI = dry matter intake (kg/day); GEI = gross energy intake (MJ/day).

The CO_2-eq. emissions associated with concentrate feed for Low and High Forage diets were calculated based on 0.530 kg CO_2-eq./kg and 0.671 kg CO_2-eq./kg respectively (Table 19).

Table 19. Carbon dioxide equivalent emissions (kg CO_2-eq.) and land use (m^2) associated with 1 kg bought-in concentrate feed for Low and High Forage diets

	Total		Low Forage			High Forage	
Component	kg CO_2-eq./kg [*]	%	kg CO_2-eq. [†]	m^2 [*]	%	kg CO_2-eq. [†]	m^2 [*]
Wheat	0.710	44.2	0.358	0.664	30.0	0.243	0.450
Sugar beet pulp	0.007	27.1	0.028	0.002	-	-	-
Soyabean meal	0.557	28.7	0.237	0.850	-	-	-
Rapeseed meal	0.642	-	-	-	45.0	0.333	0.669
Barley	0.620	-	-	-	25.0	0.180	0.425
Total kg CO_2-eq./kg			0.530	1.517		0.671	1.544

[*] Obtained from Nielsen *et al.* (2003) and adapted using mass and price allocation from Cederberg and Mattsson (2000).

[†] Based on 7.42 kg CO_2-eq/t and 141.03 kg CO_2-eq/t per 1000km for transport by sea and road respectively (Lovett *et al.,* 2006), and processing emissions of 63.3 kg CO_2-eq/t (adapted from Nielsen *et al.* (2003) and Lovett *et al.* (2006)).

These CO_2-eq. values include emissions from processing and transport from site of production to the farm. It was assumed that soyabean meal originated from Brazil, and that once in the UK all feed components travelled 250 km via the processing plant in Dumfries (Scotland) to the farm (H. McClymont, *pers. comm.*). To take advantage of the CO_2-eq. emission and land use values in Nielsen *et al.* (2003), the Low and High Forage diets were simplified to their main components, which were wheat, barley, sugar beet pulp, soyabean meal and rapeseed meal (Table 19). The barley component and wheat in the High Forage diet were fed in the form of dark grains (a by-product of whisky distilling). As only a trivial amount of processing is required for this by-product, any additional CO_2-eq. emissions were assumed to be zero. The High Forage diet consisted entirely of feed not suitable for human consumption, in the form of by-products and pasture; whereas the concentrate feed in the Low Forage diet was 31% wheat grain per kilogram DM, and may well have been suitable for humans.

The area of land required by each system depended on the forage intake (pasture, grass silage, maize silage and ammonia treated wheat silage) requirement of the milking cow

and its replacement, as well as that associated with bought-in concentrate feed as discussed above (obtained from Nielsen *et al.* (2003); Table 19). Land use was expressed in hectares per animal. The yield, fertiliser and slurry application rate associated with forage production per hectare were: 10 t DM, 150 kg N, 90 m^3 for grass silage, 10.2 t DM, 0 kg N, 45 m^3 for maize silage, 11 t DM, 0 kg N, 30 m^3 for ammonia treated wheat silage and 10 t DM, 150 kg N, 90 m^3 for pasture production respectively (H. McClymont, *pers. comm.*). Land used for forage can also act as a methane sink, as methane is oxidised within aerobic soils (Boeckx and van Cleemput, 2001) at rates shown in Table 18. Fuel use was assumed to be: 0.22 L/ha (pasture, arable management), 0.003 L/t (slurry application) and 0.8 L/t (feeding) (Lovett *et al.*, 2006).

5.3.5 Records and analysis

Data were obtained from 5,658 records from 458 cows during the study period of which 1,479, 1,288, 1,516 and 1,375 were for Low Forage Control, Low Forage Select, High Forage Control and High Forage Select cows respectively. Each record was an average over a stage interval of 60 days. Predicted means for the traits of interest were obtained using a linear mixed model. The data were analysed using Genstat Version 11.1 (Lawes Agricultural Trust, 2009) and Restricted Maximum Likelihood (REML). Cow identity was added as a random effect to allow for covariance between subsequent lactations of the same cow. Cow live weight was also added as a regression effect (excluded from the live weight model) as shown below:

$$Y_{ijklmn} = \mu + L_i + S_j + F_k \times G_l + Yr_m + M_n + C_{ijklmn} + \beta(LWGT)_{ijklmn} + E_{ijklmn}$$

where, Y_{ijklmn} = DM intake (kg/day), GE intake (MJ/day), dietary crude protein (g/kg DM), ECM yield (kg/day), milk fat content, milk protein content (both g/kg), nitrogen excretion rate (kg N/day), live weight (kg), calving interval length (days) and risk of involuntary culling (%); μ = overall mean; L_i = fixed effect of lactation number (1, 2, 3 and 3+); S_j = fixed effect of state (s) (1 to 10 states of stage intervals of 60 days over the

lactation); F_k = fixed effect of feeding system (Low Forage or High Forage); G_l = fixed effect of genetic line (Control or Select); Yr_m = fixed effect of year of calving; M_n = fixed effect of month of calving; C_{ijklmn} = random effect of cow; $\beta(LWGT)_{ijklmn}$ = regression effect of cow live weight; E_{ijklmn} = random error term.

Fixed effects of lactation number (prior to lactation four) and feeding system × genetic lines were used to model for the risk of involuntary culling. Predicted mean DM intake, GE intake, ECM yield and nitrogen excretion rate were obtained from the interaction between lactation number, state and feeding system × genetic lines. Predicted mean calving interval lengths were obtained from the interaction between lactation number and state. The predicted mean values for DM intake, GE intake, ECM yield and nitrogen excretion were modelled across states using a quadratic polynomial, as predicted means for some production systems towards later states of a lactation were missing. The shape of the polynomial curve for each trait was not adjusted.

5.3.6 Improved efficiencies of production

The sensitivities of the CO_2-eq. emissions and land use per kg ECM and CO_2-eq. emissions per hectare associated with each production system within the herd were assessed by a phenotypic standard deviation improvement of four traits (representing production and fitness traits), as well as the proportion associated with any genetic improvement. A change of one phenotypic standard deviation unit in each of the chosen traits was chosen as the fairest basis on which to evaluate the impact on CO_2-eq. emissions and land use of changes effected by any means. A change of one genetic standard deviation unit is the equivalent basis on which to compare the impact of changes brought about as a result of selection. The four traits and their heritability obtained from previous studies on the Langhill herd were: daily DM intake (average of 0.40 from Veerkamp *et al.* (1995) and Veerkamp and Brotherstone (1997)), daily ECM (average of 0.395 from Veerkamp *et al.* (1995) and Veerkamp and Brotherstone (1997)), calving interval (0.09 from Pryce *et al.* (1999)) and risk of involuntary culling during

lactation 1, 2 or 3 (0.026 from Veerkamp *et al.* (2001) based on national data for all cows culled). The herd phenotypic standard deviation (σ_p) for each trait across lactations, states and production systems were determined using the linear mixed model above, with the genetic standard deviation (σ_a) being derived by the formula:

$$\sigma_a = \sigma_p \times h$$

where h is the square root of the heritability. The traits for which a standard deviation change was modelled were:

1. Daily DM intake whilst maintaining the same ECM yield, representing an improvement in feed utilisation efficiency;
2. ECM yield whilst maintaining the same level of daily DM intake, representing an improvement in productivity;
3. Calving interval length to have a higher proportion of cows with a calving interval of between 361 and 420 days (s = 7) of each lactation rather than later than 420 days (s = 8, 9 or 10), representing an improvement in fertility;
4. Probability of being culled during either lactation 1, 2 or 3, representing a reduction in involuntary culling and improved survival to lactations 3+.

A phenotypic or genetic standard deviation change in predicted mean daily DM intakes and ECM yields were made to modelled values across lactation numbers, states and production systems before the Markov chain long-run state probabilities were applied. Changes to calving and culling data were applied to input data to the Markov chain, prior to obtaining the long-run state probabilities. Weighted average calving interval lengths were obtained for each lactation and production system, based on the herd's predicted mean calving interval length for each state within lactation and the percentage of cows calving during each state. The weighted average calving interval was then changed by a standard deviation to create a new average, represented by an equal adjustment to the percentage of cows calving during states later than 420 days (s = 8, 9 or 10) to between 361 and 420 days (s = 7), reflecting better fertility performance within

the herd. The phenotypic or genetic standard deviation change in probability of involuntary culling was applied to a lactation (1, 2 and 3) due to the low number of cows culled in each state. A standard deviation improvement in herd feed utilisation efficiency, ECM yield, calving interval length and involuntary culling was also assessed for its effect on the CO_2-eq. emissions from all sources. The CO_2-eq. emissions per kg ECM and per hectare from each source associated with the production systems studied were also determined.

5.4 Results

5.4.1 Differences between production systems

Table 20 shows the difference in production values of milking herd animals and important input variables from farm data for estimating the CO_2-eq. emissions and land use associated with the systems evaluated in this study. The non-grazing Low Forage Select genetic line cows yielded the most ECM and excrete more kilograms of nitrogen per day than other production systems studied (both $P < 0.05$). Cows on a non-grazing Low Forage system and those of Select genetic line had a significantly higher DM intake, GE intake, daily ECM yield, nitrogen excretion rate and live weight than High Forage fed or Control genetic line animals, respectively (all $P < 0.001$). Select genetic line animals had on average a higher fat and protein content in their milk compared to Control genetic line animals (both $P < 0.001$). High Forage fed animals had a significantly higher milk fat content ($P < 0.001$) and calving interval ($P < 0.01$) than those on a Low Forage diet. There was no significant difference in the risk of involuntary culling during lactations 1, 2 or 3 between production systems. However, Table 20 does show that, on average, there was a higher tendency for High Forage Control cows to be culled for involuntary reasons during lactations 1, 2 or 3 and a lower tendency for High Forage Select cows compared to the other production systems studied.

Table 20. Differences between production systems* in terms of their predicted mean production values from the farm data

Treatment		Dry matter intake	Gross energy intake	Dietary crude protein	Energy corrected milk yield	Milk fat content	Milk protein content	Nitrogen excretion rate†	Live weight	Calving interval	Involuntary culling during lactations 1, 2 and 3
		kg/day	MJ/day	g/kg DM	kg/day	g/kg	g/kg	kg N/day	kg	days	%
Feeding system	LF	19.5	374	199	28.1	38.2	33.8	0.47	693	397	23.6
	HF	18.4	337	200	22.7	40.5	34.1	0.45	670	409	22.3
	SED	0.18***	3.73***	0.52	0.36***	0.42***	0.19	0.01***	4.29***	4.86**	3.09
Genetic line	Control	18.0	333	200	23.1	38.6	33.2	0.45	672	401	24.6
	Select	19.9	378	199	27.7	40.0	34.7	0.47	690	404	21.3
	SED	0.17***	3.78***	0.51	0.36***	0.45***	0.20***	0.01***	4.77***	4.71	3.09
Feeding system × genetic line	LFC	18.4	351	200	25.5	37.3	32.9	0.45	686	395	22.5
	LFS	20.5	398	199	30.8	39.1	34.7	0.49	699	398	24.6
	HFC	17.7	317	200	20.8	40.0	33.4	0.45	658	407	26.7
	HFS	19.2	357	199	24.6	41.0	34.7	0.46	681	411	17.9
	SED	0.25	5.27	0.65	0.50*	0.60	0.27	0.01*	6.29	6.69	4.37

* LFC = Low Forage Control, LFS = Low Forage Select, HFC = High Forage Control and HFS = High Forage Select; † Nitrogen excretion rate refers to the loss of dietary nitrogen in feces and urine; SED = standard error of the difference between means; *** $P < 0.001$, ** $P < 0.01$, * $P < 0.05$.

The herd phenotypic standard deviation used to assess changes in daily DM intake (feed efficiency), ECM yield, calving interval length and involuntary culling were 2.2 kg/day, 5.4 kg/day, 18.1 days and 6.2% respectively. The corresponding genetic standard deviations used to assess a change in each of the four traits were 1.4 kg/day, 3.4 kg/day, 5.4 days and 1.0% respectively. The Markov chain results highlight that the herd structure is skewed towards lactation one cows and within lactation towards those in the earlier states of the calving interval, with a steep drop beyond state 7 (420 days) (Table 17). Distinctions between production systems are comparatively small, although the Low Forage Control group does have a higher proportion of the herd in more productive states, with the exception of lactation 4. The non-grazing Low Forage Select system had the highest overall CO_2-eq. emissions of all four production systems. The total emissions per year and land use per cow for each production system were: 10,934 kg CO_2-eq. and 0.69 ha, 11,894 kg CO_2-eq. and 0.74 ha, 10,446 kg CO_2-eq. and 0.94 ha and 11,301 kg CO_2-eq. and 1.00 ha for Low Forage Control, Low Forage Select, High Forage Control and High Forage Select systems respectively. The Low Forage Select production system had the lowest CO_2-eq. emissions per kg ECM by at least 11% (Fig. 9).

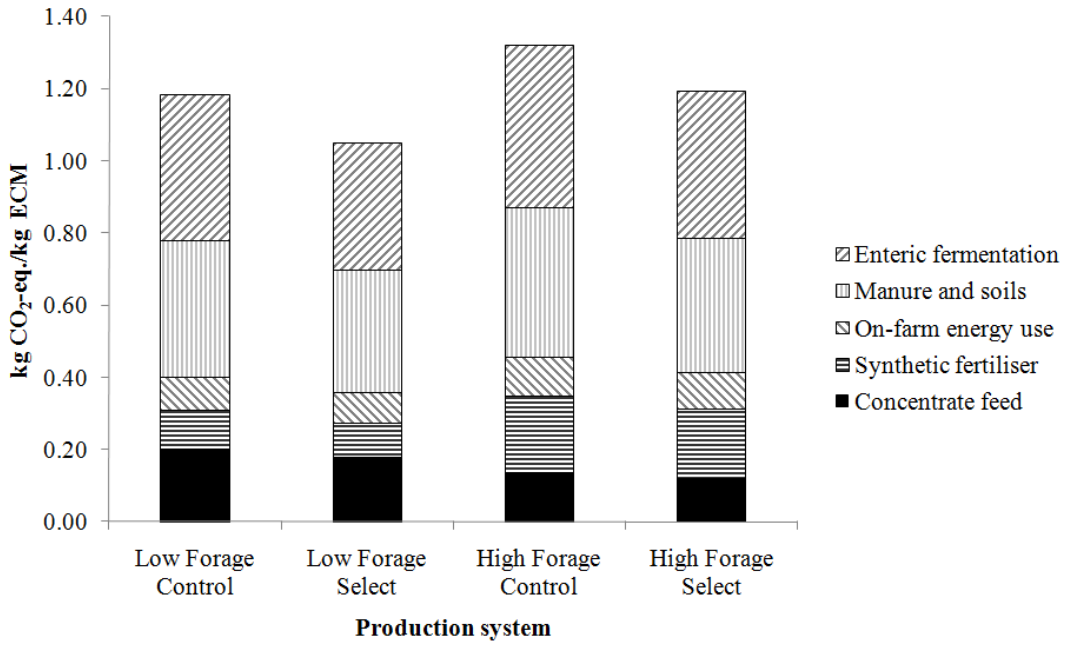

Fig. 9. Kilograms of carbon dioxide equivalent (CO_2-eq.) emissions per kg energy corrected milk (ECM) associated with each production system studied and the relative contribution from enteric fermentation, manure and soils, on-farm energy use, synthetic fertiliser and concentrate feed.

The largest contribution to the CO_2-eq. emissions per kg ECM and hectare across production systems came from enteric fermentation (34%), followed by manure and soils (32%). On-farm energy use (8%), synthetic fertiliser (9% and 16% for Low Forage and High Forage diets, respectively) and concentrate feed (17% and 10% for Low Forage and High Forage diets, respectively) made lesser but still important contributions (Fig. 9 and 10). The non-grazing Low Forage system resulted in CO_2-eq. emissions per hectare on average of at least 30% higher than a High Forage feeding system in which cows grazed during the summer months (Fig. 10). However, Low Forage systems required less land per kg ECM (averaging 0.70 and 1.13 m^2/kg ECM respectively). There was also a higher annual ECM production per hectare from Low Forage than High Forage systems (14,391 and 8,938 respectively). The Low Forage Select system used at least 13% less land per kg ECM than other production systems studied.

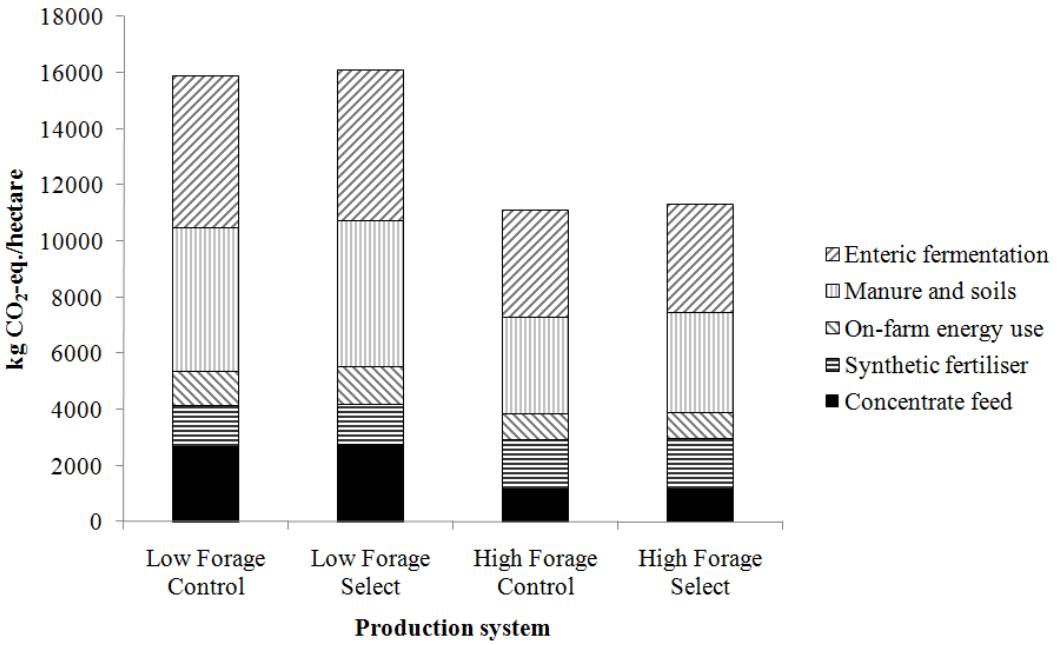

Fig. 10. Kilograms of carbon dioxide equivalent (CO_2-eq.) emissions per hectare associated with each production system studied and the relative contribution from enteric fermentation, manure and soils, on-farm energy use, synthetic fertiliser and concentrate feed.

5.4.2 Improved efficiencies of production

Fig. 11 shows that a one standard deviation improvement in feed utilisation efficiency would be the only trait of those studied that would reduce the average CO_2-eq. emissions of the herd. A reduction of 6.5% in CO_2-eq. emissions per year (4.1% per genetic standard deviation change) was seen in the average overall CO_2-eq. emissions of the herd, as well as a reduction in the need for bought-in fertiliser (7.3% phenotypic and 4.6% genetic) and concentrate feed (11.3% phenotypic and 7.2% genetic). Even though improvements in average ECM yield, calving interval length and involuntary culling did not reduce the average CO_2-eq. emissions of the herd, and indeed caused a slight overall increase (Fig. 11), reductions in system emissions per kg ECM are possible (Fig. 13).

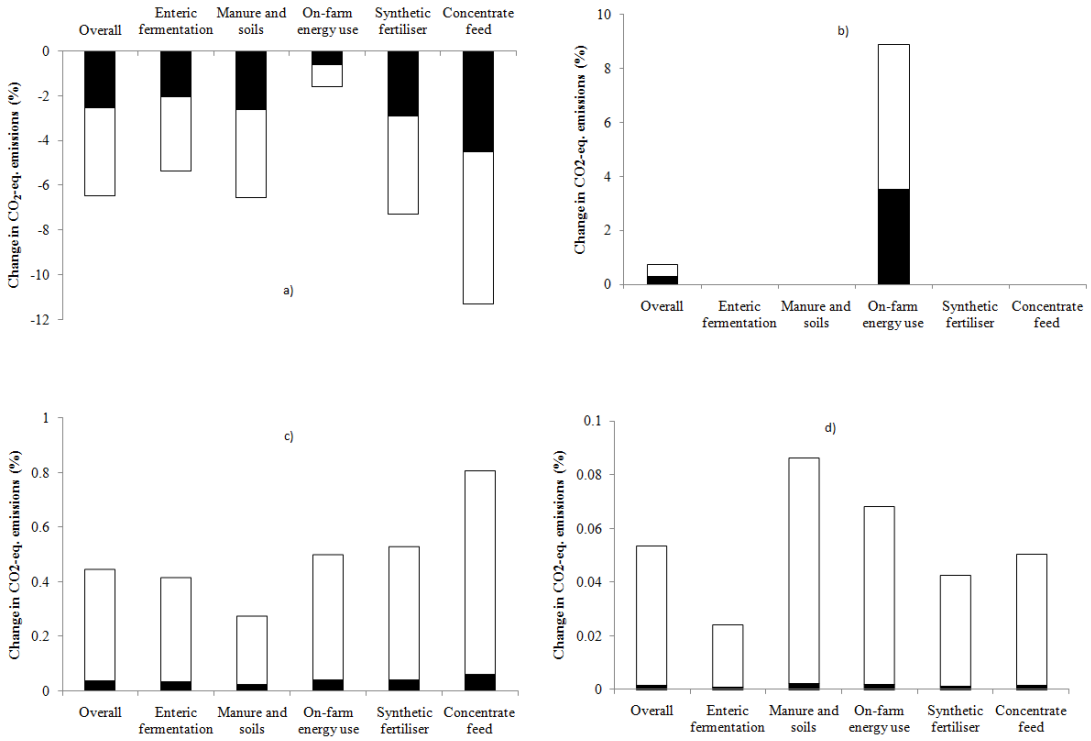

Fig. 11. Percentage change in herd carbon dioxide equivalent (CO_2-eq.) emissions associated with all sources (overall), enteric fermentation, manure and soils, on-farm energy use, synthetic fertiliser and concentrate feed sources as a result of a single phenotypic (□) and genetic (■) standard deviation improvement in a) feed utilisation efficiency b) energy corrected milk yield c) calving interval and d) involuntary culling.

Improving a cow's feed utilisation efficiency, whilst maintaining the same level of milk production, is also the best way of reducing the land use required per cow compared to the other traits studied (Fig. 12), with a one phenotypic standard deviation improvement in feed utilisation efficiency resulting in a 6.7% reduction in land use per cow (4.2% reduction per genetic standard deviation change).

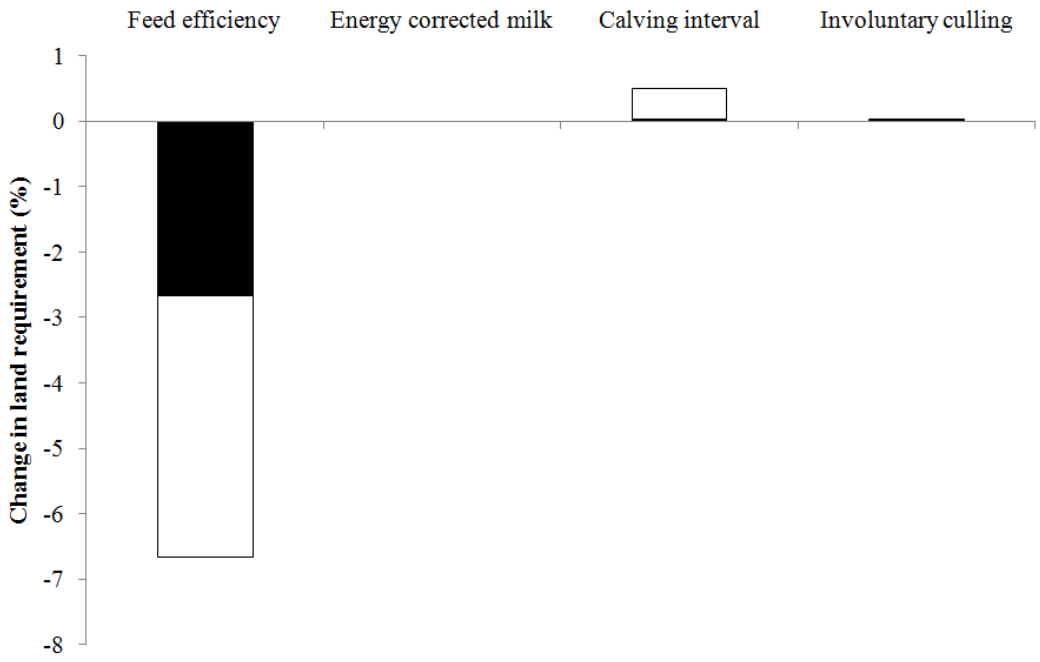

Fig. 12. Percentage change in the average land area required per cow for feed as a result of a single phenotypic (□) and genetic (■) standard deviation improvement in feed utilisation efficiency, energy corrected milk yield, calving interval and involuntary culling.

Improving the utilisation of feed within a system by one phenotypic standard deviation was also an effective way to reduce the CO_2-eq. emissions per kg ECM (Fig. 13), with a 6.0% to 6.9% reduction in CO_2-eq. emissions per kg ECM across all systems (3.8% to 4.4% per genetic standard deviation change). Fig. 13 also shows that the greatest reduction in overall CO_2-eq. emissions per kg ECM compared to an equivalent improvement in other traits studied was from a standard deviation increase in ECM yield, with the largest reductions being in the least productive High Forage Control system. Reductions ranged from 14.3% to 17.0% (phenotypic) and 9.5% to 13.2% (genetic). Reducing the herd's average calving interval by a standard deviation had a small effect on reducing the CO_2-eq. emissions per kg ECM of the production systems studied, with the Low Forage Control system showing the largest reduction of about 0.8% (about 0.2% per genetic standard deviation change). Nor would reducing the risk of involuntary culling have a significant effect on reducing the CO_2-eq. emissions per kg

ECM within each production system, with Select genetic line animals showing the main reductions of about 0.13% and 0.16% for Low and High Forage animals respectively.

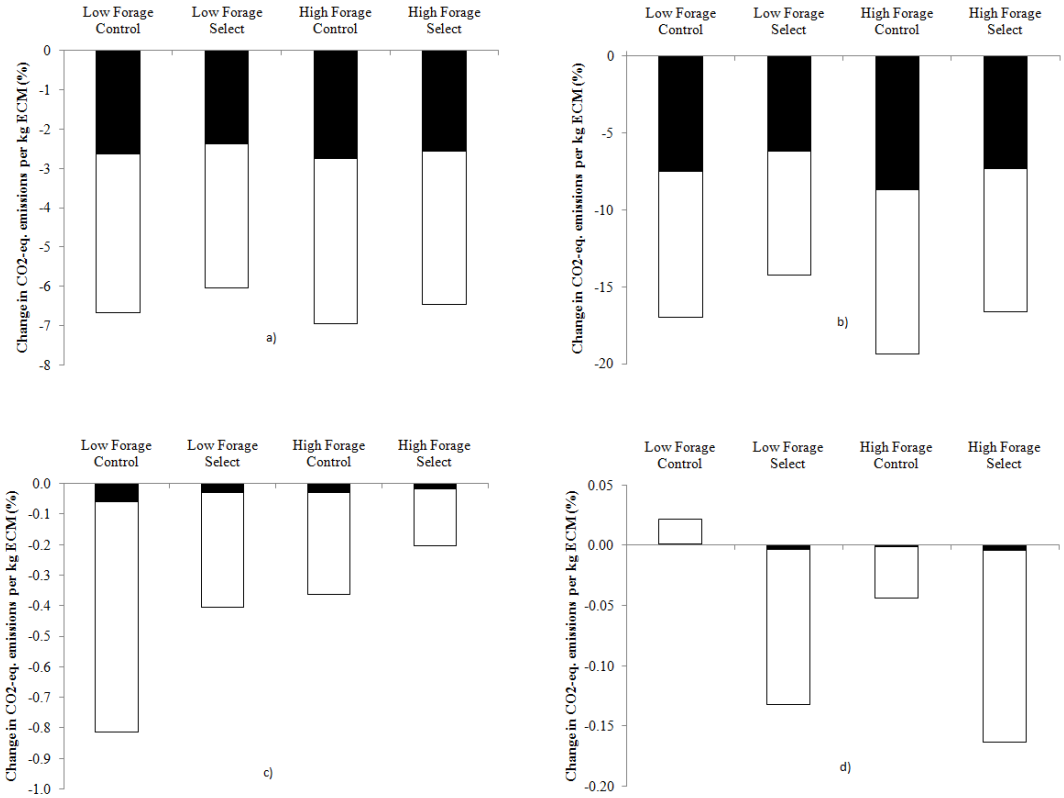

Fig. 13. Percentage change in system carbon dioxide equivalent (CO_2-eq.) emissions per kg ECM as a result of a single phenotypic (□) and genetic (■) standard deviation improvement in a) feed utilisation efficiency b) energy corrected milk yield c) calving interval and d) involuntary culling for each production system studied.

Reducing daily DM intake of cows on a High Forage diet whilst maintaining the same ECM yield led to a slight increase of 0.8% in CO_2-eq. emissions per hectare whereas cows subject to the same treatment but on a Low Forage diet showed a similar reduction (Fig. 14). This effect was due to the emissions associated with inputs, such as on-farm energy use and synthetic fertiliser to the system. Improving the ECM yield of cows resulted in an increase in CO_2-eq. emissions per hectare across all systems. A similar improvement in calving interval length showed small reductions in High Forage fed

animals of 0.16% and 0.25% for Control and Select animals respectively but only 0.02% in Control genetic line animals as a result of reduced involuntary culling.

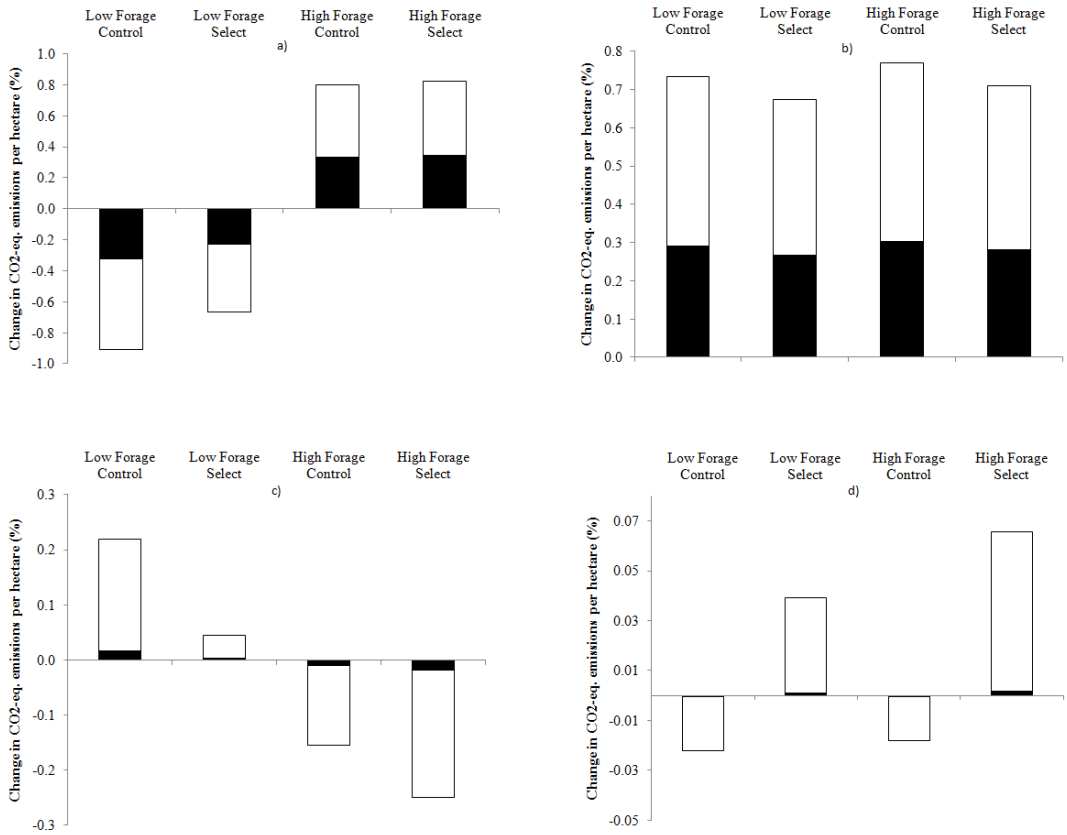

Fig. 14. Percentage change in system carbon dioxide equivalent (CO_2-eq.) emissions per hectare as a result of a single phenotypic (□) and genetic (■) standard deviation improvement in a) feed utilisation efficiency b) energy corrected milk yield c) calving interval and d) involuntary culling for each production system studied.

Land use requirements per kg ECM were also reduced within all production systems studied but more by an improvement in ECM than feed utilisation efficiency (Fig. 15). The largest reduction in land use per kg ECM by a one standard deviation increase in ECM yield was seen in the least productive High Forage Control system (20.0% reduction with 14.0% per genetic standard deviation change). In the same system improved feed utilisation efficiency resulted in a 7.7% reduction (with 4.9% per genetic standard deviation change). In comparison, the most productive Low Forage Select

system had the smallest but still significant percentage reduction in land use per kg ECM of 14.8% (with 9.9% per genetic standard deviation change) and also with regard to feed utilisation efficiency at 5.4% (with 3.4% per genetic standard deviation change). A similar level of improvement in calving interval length and risk of involuntary culling had less of an impact on land use per kg ECM than feed utilisation efficiency and ECM yield changes. The Low Forage Control, Low Forage Select and High Forage Control animals showed a reduction of between 0.2% and 1.0% for an improved calving interval length, and Low and High Forage Select animals showing a 0.17% and 0.23% reduction as a result of an improvement in the risk of involuntary culling.

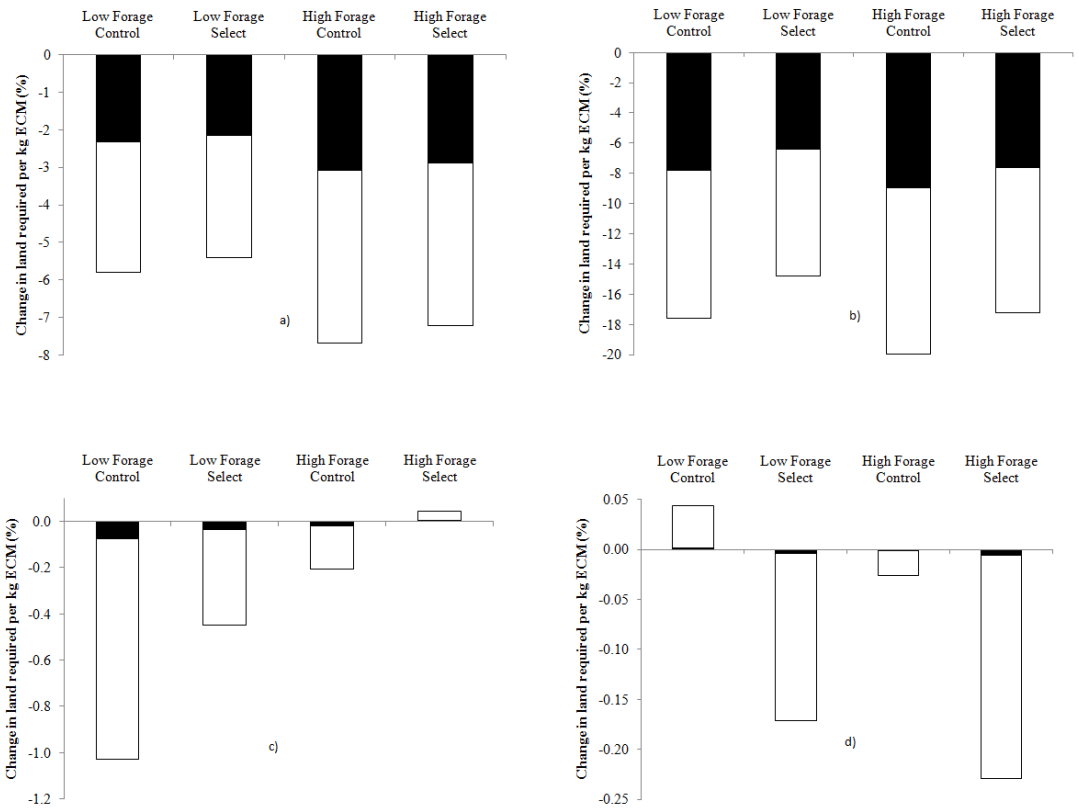

Fig. 15. Percentage change in system land requirement for feed per kg ECM as a result of a phenotypic (□) and genetic (■) standard deviation improvement in a) feed utilisation efficiency b) energy corrected milk yield c) calving interval and d) involuntary culling for each production system studied.

5.5 Discussion and conclusions

The dairy production systems within the Langhill herd, which were evaluated in this study, were designed to represent a range of dairy systems. Dairy systems with cows suited to high inputs and with a high genetic potential for milk production have become increasingly common. There has consequently been an increase in the adoption of non-grazing systems (Haskell *et al.*, 2006), so cows can meet their energy requirements using high energy dense concentrate feeds with its associated increased digestibility and rumen fermentation rate. Cows with North American Holstein-Friesian genes have been found to show a better response in milk yield to concentrate feed in their diet than a genotype like the New Zealand Holstein-Friesian, which has been selected for higher milk yield performance from pasture (Dillon, 2006a). O'Brien *et al.* (2010) found that the New Zealand Holstein-Friesian cows managed with a high stocking rate were more suited to a low input pasture-based system, whereby they were more profitable and with lower GHG emissions than cows of North American Holstein genes on this type of system. However, pasture can vary much more in quality compared to blended concentrate feed, or even conserved forages used in a total mixed ration. A poorer quality food can impair the energy intake and potential milk yield of the animal, as can the cow's inability to achieve desired pasture DM intake (Dillon, 2006a; Dillon *et al.*, 2006b). Pasture can also vary in its availability but when available it is generally more affordable than blended concentrate feed. Therefore it is important to not only consider the impact in CO_2-eq. emissions per unit product (per kg ECM) but also per hectare of land required for feed.

On average the non-grazing low forage fed cows in this study, predominantly of North American Holstein genetic background, produced 15% more milk each day per kg DM intake and required 26% less land for forage and concentrate feed than systems utilising pasture. The higher productivity associated with a non-grazing system in the present study meant a higher CO_2-eq. emissions per hectare compared to other production systems in this study or other studies on intensive dairy systems (Table 21). The differences between studies in their reported CO_2-eq. emissions per kg ECM and per

hectare and land use per kg ECM shown in Table 21 reflect the variation in intensive systems evaluated. Basset-Mens *et al.* (2009) found that the CO_2-eq. emissions and land use per kg ECM for the average New Zealand Holstein-Friesian dairy system, presented in Table 21, could be further reduced to 0.65 kg CO_2-eq./kg ECM and 0.74 m^2/kg ECM respectively with lower inputs to the current Holstein-Friesian pasture-based systems typically found in New Zealand, which would result in lower values than those seen in other studies. Basset-Mens *et al.* (2009) suggested that New Zealand's pasture-based systems could rely almost entirely on natural resources rather than bought-in farm inputs in addition to having a lower environmental impact as mentioned above. In comparison to this study, the study by Basset-Mens *et al.* (2009) included capital items such as buildings and machinery, which were not included in the present study as it assessed production systems within the same farming unit.

Table 21. Comparison of the carbon dioxide equivalent (CO_2-eq.) emissions per kilogram energy corrected milk (ECM) yield and per hectare (t/ha) and land use (m^2) per kilogram ECM of Langhill herd production systems to other intensive dairy system studies

	CO_2-eq. emissions		Land use
Study	kg/kg ECM	t/ha	m^2/kg ECM
Non-grazing Low Forage Control	1.18	15.9	0.75
Non-grazing Low Forage Select	1.05	16.1	0.65
High Forage Control	1.32	11.1	1.19
High Forage Select	1.19	11.3	1.06
Cederberg and Mattsson (2000)	1.10	5.7	1.93
Haas *et al.* (2001)	1.30	9.4	-
Casey and Holden (2005)	1.51	-	-
Thomassen *et al.*(2008)	1.41	11.0	1.28
Basset-Mens *et al.* (2009)	0.96	8.1	1.05

The present study showed that management and breeding for improved feed utilisation would be the most effective way of reducing the CO_2-eq. emissions, land use, CO_2-eq. emissions and land required per kg ECM of the systems studied. By improving the feed use within a system, the CO_2-eq. emissions associated with bought-in resources such as fertiliser and concentrate feed can be reduced (by 7% and 11% respectively). Casey and Holden (2005) and Thomassen *et al.* (2008) found that better farm nutrient and pasture management would reduce the CO_2-eq. emissions of dairy systems by minimising the need for bought-in fertiliser and concentrate feed. In this study there was only a slight

change in the CO_2-eq. emissions per hectare of each production system studied as a result of an improvement in feed utilisation efficiency, as emissions per hectare reflect the efficiencies of use of inputs to the system (i.e. on-farm energy use and synthetic fertiliser) as found by Basset-Mens *et al.* (2009). A reliance on bought-in concentrate feed, which can be costly, has an additional environmental impact depending on the feed and whether it was a by-product or not. The cows on a low forage diet in this study may have a lower CO_2-eq. emissions and land requirement per kg ECM than cows on a high forage diet, however, the high forage diet consisted entirely of feed products that are not suitable for human consumption (pasture and by-products from the brewing and distilling industries). There is no reason why the feed used in the low forage diet fed in this study should not also be sourced from products not suitable for human consumption. It is more efficient to utilise crops that are suitable for human consumption directly rather than as a livestock product (Gill *et al.,* 2009). Also, by-products such as brewers' grains, distillers' dark grains and draff from the brewing and distilling industries, have a relatively low methane output as a percentage of GE compared to other feed products (Wainman *et al.,* 1984) and form a useful source of low CO_2-eq. emission nutrients for dairy cows. The impact of feeds from different sources was not included in the analysis due to more information being required before this can be included as an impact category. This study standardised the CO_2-eq. emissions for concentrate components of the diets fed, whereas in reality distances travelled and feed components used will vary between farming systems and affect the CO_2-eq. emissions associated with bought-in feed.

The present study showed that 66% of the CO_2-eq. emissions from a dairy system per kg ECM and hectare are from methane and nitrous oxide emissions, through enteric fermentation, manure and soil sources, i.e. as a result of the on-farm nutrient utilisation of the animal. Yan *et al.* (2010) found that selecting cows with high energy utilisation efficiencies and milk productivity offers an effective way of reducing enteric methane emissions. Chapter 3 shows that selection for increased milk fat and protein yield can reduce dairy system methane emissions and non-milk nitrogen yield per kg milk

(Chagunda *et al.*, 2009), even though high milk yielding cows are associated with higher emissions per animal. Increasing the genetic capacity of the animal to produce more milk will increase total GHG emissions from a dairy system. However, CO_2-eq. emissions per unit product can be reduced, as was shown by Lovett *et al.* (2006) and seen in this study. The reduction in CO_2-eq. emissions per unit product is due to high milk producing cows (i.e. Select genetic line) having a higher GE efficiency than lower milk producing cows (Wall *et al.*, 2010a), which is optimised when mature size and maximum milk production is reached (van de Haar and St Pierre, 2006). A study by van de Haar and St Pierre (2006) found that when maximum energetic efficiency is reached, environmental waste (in the form of methane and nitrogen excretion) will be minimised per unit product. Management and breeding for increased productivity (daily ECM yield) can have a large impact on reducing the CO_2-eq. emissions and land use requirement per kg ECM whilst maintaining the same level of DM intake, although there was a slight overall increase in the CO_2-eq. emissions per hectare. As mentioned above, to maximise the genetic potential of a high milk producing cow high energy dense diets in the form of a total mixed ration are usually fed in a controlled area. Selection for improvements in production efficiencies (i.e. the ratio of yield of milk to resource input) with regard to nutrient partitioning and feed intake has a major potential for reducing the GHGs of dairy systems (shown in Chapter 3 and found by Bauman *et al.*, 1985). Also, cows with a high live weight, such as non-grazing Low Forage Select animals in this study, have been found to have a greater bite weight when eating and therefore to be more efficient in their use of time spent feeding (Dillon, 2006a). In addition to animal efficiencies, the housed environment offers a potential source of electricity from manure methane emissions, provided the manure storage area is kept gas-tight (Clemens *et al.*, 2006). There are well established techniques such as anaerobic digestion (Cantrell *et al.*, 2008) which could capture and utilise the methane emissions associated with manure from a housed environment. This could potentially offset some of CO_2-eq. emissions associated with energy use, and reduce manure contributions to GHG emissions (Clemens *et al.* (2006).

Of the traits assessed in this study, increasing feed utilisation efficiency and ECM yield (production traits) had more of an effect on reducing the environmental impact of the production systems evaluated compared to improvements in the fitness traits of calving interval length and risk of involuntary culling. As a result of efficient production, healthy and fertile cows do however offer savings in GHGs per unit product (Garnsworthy, 2004). The results in this study associated with the risk of involuntary culling may be affected by the experimental protocol, as cows are required to be kept in the herd for at least three lactations unless welfare dictates that culling is necessary. In contrast to the study by Garnsworthy (2004) where a higher proportion of forage in the diet was fed with an extended lactation, the cows in this study remained on the same diet throughout their lactation and a fixed lactation curve was assumed for a 600 day calving interval. Results in Chapter 3 showed that an increasing forage proportion in the diet will increase the proportion of energy intake lost as methane and increase methane output per unit product. Therefore, the large reduction in methane emissions reported by Garnsworthy (2004) as a result of improving fertility performance at the herd level could be higher than you would necessary be able to achieve in practice. Cows in each production system in this study showed a slight reduction in CO_2-eq. emissions per kg ECM with an improvement in fertility as a result of more animals moving to more productive stages of the lactation.

In conclusion, cows selected for increased milk fat and protein yield (i.e. Select genetic line) rather than to represent the UK average (i.e. Control genetic line), were not compromised in this study by their fertility performance and risk of involuntary culling whilst on a high or low forage diet; therefore, there was minimal impact on the CO_2-eq. emissions per kg ECM and per hectare, as well as land use per kg ECM seen in the production systems studied compared to other traits studied. The CO_2-eq. emissions per kg ECM of Control genetic line cows would benefit slightly more than Select genetic line animals by further improvements in ECM yield and feed utilisation efficiency. In this study, a non-grazing Low Forage feeding system with Select genetic line cows had the lowest CO_2-eq. emissions per kg ECM and land use per kg ECM, but the highest

CO_2-eq. emissions per hectare of the production systems studied. If a high forage production system is more economical or health and welfare concerns associated with a non-grazing system dictate that a period at pasture is preferential, then future policy should look to select dairy genotypes with improved feed utilisation efficiency for milk production on a high forage rather than a low forage diet. Improved feed utilisation efficiency in dairy cows could also significantly reduce the reliance of the farming system on bought-in synthetic fertiliser and concentrate feed. Future work could incorporate health, welfare and feed source as impact categories in a whole system model.

Chapter 6 General discussion and conclusions

The aim of this research was to investigate mitigation options with regard to GHG emissions from dairy systems, with an emphasis on methane. The extensive and detailed data from the production systems within the Langhill experimental herd were used as a means to assess dairy system mitigation options. The findings of this study are discussed below in terms of how they relate to adaptations and strategies to mitigate emissions on a national scale.

The UK is a significant producer of milk, being the third largest milk producer in the European Union and the ninth largest in the world (House of Commons Library, 2010). Garnett (2009) suggested that to bring about reductions in livestock GHG emissions, significant technological and managerial innovation will be required, in addition to reducing our consumption of meat and milk products. It is well recognised already that dairy production has made large advances in efficiencies over the past 60 years as a result of changes in breeding, nutrition and management practices (Capper *et al.*, 2009). With these advances have come reductions in the environmental impact of dairy systems in terms of GHG emissions and land required per unit product (Capper *et al.*, 2009). However, losses of dietary energy in the form of methane, as well as nitrogen in manure, are still significant inefficiencies associated with livestock production systems, which can impact on the environment.

In the absence of methane measurements, this study relied on enteric and manure methane prediction equations to estimate emissions. As you would expect, more recent prediction equations for enteric methane output, which were developed on a broad range of input values, were found to be more suitable for the range of values seen in data from the Langhill herd, which was the focus of this study. Therefore, suitable methane prediction equations for the Langhill herd data would also be suitable for production values that could be found in the commercial Holstein-Friesian population. By testing

methane output prediction equations outside the range of values on which they were developed, some equations give unrealistic predictions. The main difference amongst the performances of methane prediction equations is their ability to give a sensible estimate at low DM intakes, which is a common occurrence in commercial systems when animals may not be eating properly. At higher DM intakes, differences amongst equations in their prediction of methane output are more apparent. Further validation with methane measurements taken at high DM intakes are required to assess the accuracy of estimates. Logically, some prediction equations include intake of carbohydrate as a variable (Table 3, Section 1.2.3.2), however, by increasing the complexity of an equation the prediction might be more accurate but obtaining values for input variables may be difficult, which in this case would rely on feed analysis and feed intake information. Of the equations indentified in Chapter 2 as suitable for the production values seen in the data from the Langhill herd, DM intake and nutrient intake were the important variables used. Estimating an animal's enteric methane output based on its energy requirements were found in this study to over-predict methane output, particularly during the first 11 weeks of the lactation. However, over a period of time (as when used in national inventories), such as a lactation, enteric methane production estimated using the Intergovernmental Panel on Climate Change (IPCC) Tier II methodology (1997) was found in this study to have a high and positive correlation (0.89) with that estimated from ME intake using the non-linear equation of Mills *et al.* (2003). The IPCC methodology is based on production variables that are generally more easily obtained than those used in statistical or even more dynamic enteric methane prediction equations.

6.1 Breeding for reduced emissions

On average, Holsteins of North American or European origin are more profitable in UK dairy systems due to their high milk yields (Moore *et al.*, 2010). This has resulted in Holstein genes being present in a large proportion of dairy cows in the UK (66%) (Defra, 2005), particularly those of North American or European bloodlines. Moore *et al.* (2010) found that Holsteins of North American or European origin tend to have a

more favourable Predicted Transmitting Ability (PTA) to selective breeding on production traits, rather than lifespan like UK and Oceanic bloodlines. Larger North American Holstein-Friesian cows have been found to show a better response in milk yield with a low proportion of forage in their diet than smaller genotypes like the New Zealand Holstein-Friesian, which has been selected for higher milk yield performance from pasture (Dillon, 2006a). Larger animals are also more efficient feeders, with a greater feed intake per bite compared to smaller animals (Dillon, 2006a). Cows in this study, which were on average 88% North American Holstein genes, had a faster growth rate and increased kg milk per kg DM intake during their productive life when selected for increased milk fat and production on a high energy dense diet (Select genetic line), compared to cows selected to represent the UK average for milk fat and protein production (Control genetic line). Select genetic line animals have a high genetic potential for mobilising body energy reserves for production, which has been found to have deleterious effects on health and fertility (Pryce *et al.*, 1999; Dillon *et al.*, 2006b), particularly later in life (Wall *et al.*, 2010a). Select genetic line animals have a high energetic efficiency up to their third lactation (as suggested by van de Haar and St Pierre (2006)), resulting in savings in GHG emissions per kg milk, however, over a lifetime there is no significant difference to Control genetic line animals. This study found however, that maintaining milk productivity in terms of average yield per cow can still help reduce dairy system methane emissions per unit product. Further work is required to determine the point at which Select genetic line animals no longer have significantly lower system emissions per unit product compared to Control animals, due to the effects of poor health and fertility on their longevity (Wall *et al.*, 2010a).

Further efficiencies of production were seen in this study in Select genetic line animals on a non-grazing system fed a low proportion of forage in their diet, with cows producing more milk and having improved fertility performance compared to animals fed a higher proportion of forage in their diet. Cows of predominantly North American Holstein genes may be better suited on the whole to high energy dense feeding systems, typically found in the US, rather than a diet containing a high proportion of forage.

Capper *et al.* (2009) reported good health and welfare in modern high input systems (cows of 90% Holstein genes) in the US, with better production efficiency and CO_2-eq. emissions per unit product compared to the past. This may be explained by optimal nutrition being provided to these animals, in the form of high cereal-based diets, which will be discussed further in Section 6.2 with regard to different production systems. Select genetic line animals on a non-grazing/low forage diet produce less CO_2-eq. emissions and require less land for feed per unit product than when fed a higher proportion of forage in their diet. Cows on a non-grazing system partition more of their nutrient intake towards milk production, rather than maintenance (Bauman *et al.*, 1985). However, only about 5% of UK dairy systems are non-grazing (M. Haskell, *pers. comm.*). There has been a growing trend towards cows spending less time at pasture (Haskell *et al.*, 2006) and more time in a controlled feeding area (i.e. non-grazing system) to meet their energy requirement, which for UK dairy cows is usually done in a housed environment. A non-grazing/low forage feeding system in this study was associated with higher CO_2-eq. emissions per hectare compared to a high forage based diet with summer grazing, due to the higher resource inputs required. Selecting animals on improved feed utilization efficiency could potentially reduce the reliance of the farming system on inputs such as synthetic fertiliser and concentrate feed.

Currently, feed efficiency is not included in dairy cow breeding programmes, due to the difficulties of measuring the feed intake of progeny on farms and the associated cost. Results from this study suggest that selecting on feed utilisation efficiency could be an effective way of reducing the CO_2-eq. emissions, land use, CO_2-eq. emissions and land required per unit product in dairy systems, compared to improvements in cow fertility, milk production or longevity. Hegarty and McEwan (2010) also found that significant savings could be made by selecting ruminants for improved feed efficiency. Over a lifetime, daily DM intake (0.25) and lactation period length (0.75) explained the phenotypic variation seen in system methane emissions per kg milk. Since feed intake is an important variable with regard to dairy system methane emissions and about 66% of the CO_2-eq. emissions of raw milk production come from enteric fermentation and

manure, then future breeding goals should look to include feed efficiency. The present study suggests that selection for increased milk fat and protein production has already brought large savings in enteric methane emissions per kg milk, with reductions of 19% in Select genetic line cows compared to 23% for Control genetic line cows in 1990. The large reduction in enteric methane emissions per kg milk seen in the Control genetic line cows from 1990 reflects an increase in the UK average for milk fat and protein production over time, with a 4% greater reduction in Control genetic line animals compared to that of Select. Feed intake is a heritable trait (0.40 in the Langhill herd) with a high level of between-animal variation. Hegarty and McEwan (2010) also found significant sire differences in enteric methane output in sheep, with a heritability of 0.13 (adjusted for live weight). If suggested reductions of at least 10% in enteric methane loss from DM (Eckard *et al.,* 2010) are possible and is then coupled with a genetic standard deviation improvement in feed requirement per unit product (shown in Chapter 5), methane losses from UK Holstein-Friesian dairy cows could potentially be reduced by 15% per kg milk. This estimate was based on an average intake of 18 kg DM/day and milk yield of 23.2 kg/day from the Control genetic line cows in the Langhill herd, on a low and high forage diet since 2002.

Selective breeding offers a medium to long-term approach to GHG mitigation, which can be cost effective, compared to management options (Moran *et al.*, 2007). Currently, using progeny testing, an economic Profitable Life Index (£PLI) is used in the UK to give economic weighting to the genetic improvement that a proven Holstein-Friesian sire will give to a range of production (kilograms milk, kilograms fat and protein) and fitness (lameness, mastitis, fertility[4] and lifespan) traits for UK conditions (DairyCo Breeding+, 2010). Fitness traits have a relative weighting of about 55% in the current £PLI index (DairyCo breeding+, 2010), therefore health and welfare can be expected to improve in the future through selective breeding. There is little evidence to suggest that improvements have been made in the fitness traits of lameness, mastitis or fertility since

[4] Including calving interval, non-return rate at 56 days, body condition score, milk yield at insemination, days to first insemination and number of inseminations.

1997 (FAWC, 2009). Therefore these traits still offer savings in system emissions, particularly in terms of efficiencies of production (Garnsworthy, 2004). Wall (2010b) investigated changing selection weightings in the current UK £PLI index to give more emphasis to environmental objectives; however the structure of the current UK £PLI was found to be economically and environmentally beneficial to producers. Any mitigation option needs to have a positive economic impact on animal production and farm profitability to be accepted by the industry. Genomic information could potentially make selecting animals on their feed efficiency easier and cost effective. The development of genomic breeding values rather than estimated breeding values using progeny testing offers a more cost effective approach and increased rates of genetic improvement (three to four times that of progeny testing), in addition to the potential to select animals at a young age (Schaeffer, 2006). Genomic information could also potentially increase the accuracy of current breeding values (Schaeffer, 2006) and help introduce more genetic variation back into dairy populations, which was being lost by progeny testing and use of a small number of proven sires (Kearney *et al.*, 2004). If countries were to create a pooled reference population (capturing the interaction between different genotypes and their environment) for genome-wide selection calibration studies, this would not only increase our knowledge of the biology of traits but a greater range of traits could potentially become more accurately acquired.

6.2 Matching genotypes to their environment

Genomic information could help breeding programmes match genotypes to their farm environment more effectively, which could potentially bring further reductions in system GHG emissions in the future. In this study the genetic potential for milk production of Select genetic line animals was limited by a diet with a high proportion of forage. The current approach of evaluating progeny for production and fitness traits across breeds and environments fails to fully account for the effect of environment on different genotypes, and therefore there is potential for better genetic progress to be made within different production systems. Strandberg *et al.* (2009) found a genotype by environment interaction for fertility traits, with days to first insemination and calving interval

explaining the majority of the genotype by environment variation observed. It could be that these fertility traits are more accurately acquired than traits that rely on a pregnancy diagnosis. Sires vary in the sensitivity of their daughters to different farm environments (Haskell *et al.*, 2007), as production systems can range widely in terms of feeding system, management and climate. Haskell *et al.* (2007) studied Holstein-Friesian herds and found production intensity (age at first calving, kilograms milk, milk fat and protein production) and climate (temperature and rainfall) were the factors explaining the majority of the variation seen in production systems across the UK. Several of these variables were also common variables identified in a study on Holstein-Friesian cows across countries by Zwald *et al.* (2003). Zwald *et al.* (2003) found climatic temperature, herd size, sire PTA for milk, percentage of North American Holstein genes, peak milk yield, fat to protein ratio in milk and standard deviation of milk yield to be the main variables explaining the majority of variation between a genotype and its environment. Haskell *et al.* (2007) found that the majority of sires had daughters with increased survival (affected by health and fertility) on less intensive systems, but a small proportion of sires had daughters less affected by the environment. Therefore matching a sire's genotype to a farm environment would be beneficial to the production efficiency of their daughters. This may involve identifying sires for cows on low or high input production systems (i.e. low and high resource use respectively) in different areas of the UK, or sires that produce daughters less affected by their environment. Better production performance would also help minimise the farm's environmental impact, by reducing the CO_2-eq. emissions and land required per unit product. However, any success in selecting an animal for a particular production system would be dependent on relevant detailed information being accurately recorded by breeding companies on sires and about farms in different locations.

High input systems tend to rely more on high energy dense diets rather than maximising pasture use as in low input systems. Management to optimise the utilisation of available forage and its quality is important to the profitability of any dairy system, as well as helping to minimise the proportion of energy consumed by the animal that is lost as

methane. About 55% of land in the UK is permanent pasture (Defra, 2009) and therefore large areas are suitable as an affordable source of nutrients. Organic systems in the UK are required to have no more than 40% of the diet concentrate feed on a DM basis, as well as providing cows with access to pasture (Soil Association, 2010). But pasture-based systems are more vulnerable to variable forage quality, than those using blended concentrate feed, or even the conserved forages used in high input systems. Poor quality food can impair the energy intake and potential milk yield of the animal, as can the cow's inability to achieve desired grass intake at pasture (Dillon, 2006a; Dillon *et al.*, 2006b), which can increase land required and system emissions per unit product. Lovett *et al.* (2008) and Basset-Mens *et al.* (2009) found cows selected for higher milk production at pasture, rather than on concentrate feed, had a lower environmental impact per kg milk and per hectare if the system was low input. Cows in this study of on average 88% North American Holstein genes would also have shown lower system CO_2-eq. emissions per hectare with a reduction in resource inputs, particularly that of bought-in synthetic fertilizer, which was also found by O'Brien *et al.* (2010). High forage or pasture-based systems require animals that can optimise their feed intake and utilise it effectively for milk production. Further to the study by Basset-Mens *et al.* (2009) on New Zealand Holstein-Friesians, O'Brien *et al.* (2010) found that the most profitable pasture-based system with lowest GHG emissions were New Zealand Holstein-Friesians managed with a high stocking rate rather than using North American Holstein bloodlines.

A high input system can minimise its environmental impact per kg milk by breeding cows for high milk production (i.e. non-grazing and high energy dense diet) with efficiencies associated with improved energy efficiency for milk production. Enteric methane production is positively correlated with feed intake, but the percentage of dietary gross energy lost as methane declines with increasing feed intake (Kebreab *et al.*, 2006b). Cows in this study were found to lose less of their metabolisable energy intake as enteric methane when their intake was particularly high, which is significantly higher in older animals, Select genetic line animals and those with a low proportion of forage in

their diet. High input systems are associated with greater CO_2-eq. emissions per hectare than lower input systems, but emissions could be offset by manure management to use the methane from slurry storage for energy and contain emissions released from storage and field application (Clemens *et al.*, 2006; Weiske *et al.*, 2006). Anaerobic digesters can potentially capture 68% of total methane emissions from slurry manure, with the proportion of organic matter and temperature influencing methane production (Clemens *et al.*, 2006). Future work could incorporate these aspects in a whole system model to evaluate the savings in emissions and the effect of diet manipulation.

Garnett *et al.* (2009) highlighted the higher feed conversion efficiency associated with intensive poultry and pigs (ranging from 1.7 to 2.4 kg cereal feed per kg animal weight), where profitability on cereal-based diets has encouraged selection for feed efficiency compared to ruminant systems. However, taking into account the competition between humans and animals for cereal products, Gill *et al.* (2009) found that while high inputs of cereals in US monogastric and dairy systems had brought high and efficient production, these systems were not net contributors of food for human consumption. The concentrate blend in a dairy cow's diet can consist of cereals or by-products from other industries that may or may not be suitable for human consumption. It is more efficient to utilise crops that are suitable for human consumption directly rather than as a livestock product. By-products not suitable for human consumption are used extensively in UK dairy cow diets as an affordable source of nutrients. By-products such as brewers' grains, distillers' dark grains and draff have a relatively low methane output potential per unit of GE (Wainman *et al.*, 1984). The reliance of a high input system on a resource such as bought-in concentrate feed can be costly and vulnerable to price fluctuations, compared to cheaper resources such as homegrown forage, which can vary in quality but with a lower carbon footprint (Thomassen *et al.*, 2008). This could also be said of purchased synthetic fertiliser (Casey and Holden, 2005), as well as dietary additives. Importantly, few dietary additives have as yet had a reliable affect on reducing methane production without reducing an animal's production. The most promising and cost-effective additive for reducing methane production appears to be the

addition of cellulase and hemicellulase enzymes to a ruminant's diet (Beauchemin *et al.*, 2008).

6.3 Adaptations and strategies to mitigate dairy system emissions

Dairy farming is a highly managed system and as such lends itself well to possible reductions in pollutants, such as methane emissions. Many of the strategies for minimising GHG emissions such as methane bring economic benefits to dairy farming to produce sustainable food production, via optimum animal performance and reduced inputs as shown in Fig. 16.

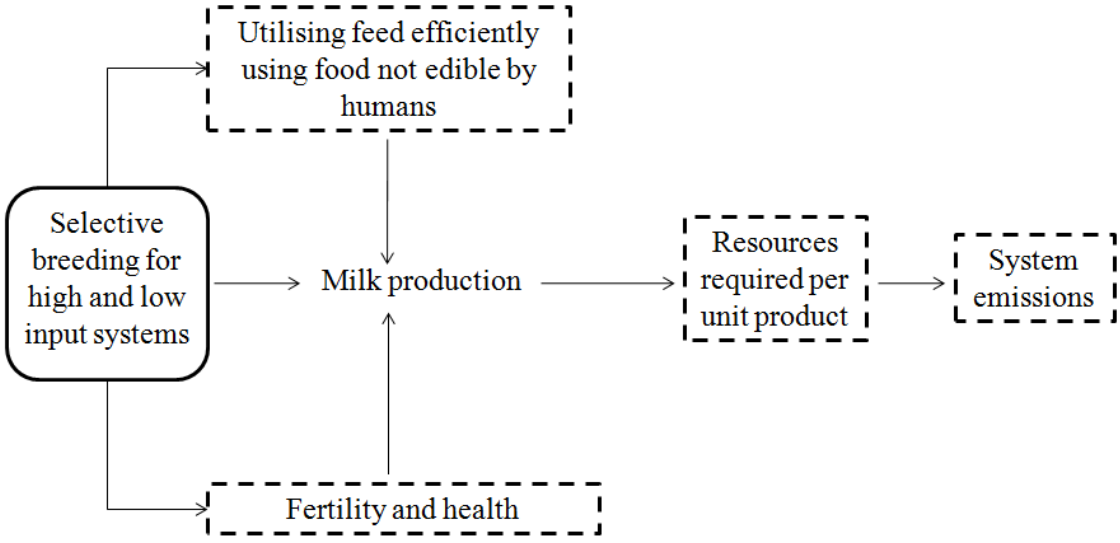

Fig. 16. Production efficiencies using management (---) that can reduce methane and overall GHG emissions beginning with selective breeding of a genotype for a particular system

This includes management to optimise milk production, age at first calving and the length of the drying off period without compromising health and fertility. Technologies that can bring affordable efficiencies to production are being developed. Using genomic information and sexed semen (Weigel, 2004) offer the potential for better selective breeding. Technologies to capture methane (anaerobic digesters), robotic milking

machines which increase milking frequency and production (Wagner-Storch and Palmer, 2003), health and fertility monitoring devices (Løvendahl and Chagunda, 2010) and practices that reduce energy expenditure (mobile milking units) can all potentially help reduce GHG emissions per unit product indirectly. Further research is required to assess the savings made in system emissions by implementing available technologies.

For dairy systems to further reduce their GHG emissions this study recommends:

1. Breeding feed-efficient animals;
2. Optimising a cow's energy efficiency for milk production without compromising its health and fertility;
3. Selective breeding of genotypes for high or low input system to improve animal performance and productivity.

Appendix A Risk factors for culling in Holstein-Friesian dairy cows[5]

A.1 Summary

The aim of this study was to identify the risk factors associated with culling (voluntary and involuntary) within a Holstein-Friesian dairy cow research herd. Data were studied from 3,498 completed lactations from January 1990 to June 2008. During this period the cows were based at two different farms in Scotland, with the culling rate of the milking herd being approximately 25% per annum. Some 68% of cows culled were classified as involuntary. The association between different risk factors and the incidence of culling were investigated using a general linear mixed model. Of the 838 cows culled, 59% were culled before the fourth lactation. With regard to the distribution of records over time, 80% of the cows that were culled were at Farm 1 and 20% at Farm 2. Culling was associated with cows that had an assisted calving ($P < 0.01$), aborted ($P < 0.01$) and/or suffered from mastitis ($P < 0.05$). Cows that were culled were also more likely to be older cows ($P < 0.01$), have a low number of milking days ($P < 0.001$) and/or a greater number of days from calving to conception ($P < 0.01$). Cows culled were also associated with conception failure ($r = 0.752$, $P < 0.001$). Further work could help reduce the occurrence of involuntary culling by identifying key factors associated with the incidence of an assisted calving, abortion, mastitis, and improving milking and fertility performance using detailed data from the Langhill herd.

Key Words: Dairy cattle, culling, factors, health, fertility.

A.2 Introduction

Modern Holstein-Friesian dairy cows are associated with increased milk production per cow, a lower body condition score, greater response of milk production to concentrate supplementation at pasture and reduced health and fertility (Dillon *et al*, 2006b).

[5] Published in The Veterinary Record (Bell *et al.*, 2010b)

Longevity in the milking herd can be influenced by management and breeding decisions, to maintain a herd size from the replacements available. Rogers *et al*. (1988) suggested that management and breeding policies should be directed towards not only increasing milk yield but decreasing the causes of involuntary culling. The level of replacements needed influences the productivity and profitability of the herd, as at a high rate the replacement costs are high but at too low a rate the milk production, reproduction or genetic improvement of the herd may be impaired (Hadley *et al*., 2006).

The objective of the present study was to identify the risk factors associated with culling using a detailed and extensive dataset over an eighteen year period.

A.3 Materials and Methods

A.3.1 Data

There were 3,498 completed lactations (from 1,205 cows) during the study period from January 1990 to June 2008. The data are described in Section 1.3.3. The herd averaged 7,506 ± 52 kg milk per lactation, with an average number of lactations of 2.7 ± 0.03 (median of 2). The incidence of culling (voluntary or involuntary) and any health problems during each lactation were recorded for each cow. Culling was classified as the time at which the cows' productive life ceased, whether it is for voluntary or involuntary reasons. An involuntary culling was classified as cows whose primary culling reason was due to a reproductive problem, foot/leg problem, udder problem including poor yield and high somatic cell count (SCC), death or abortion.

Culling and any health problems during each lactation were recorded for each cow as described in Section 1.3.3, and included in the analysis. When veterinary assistance was required, the same farm veterinarian was used where possible. Fig. 17 shows the proportion of the 3,498 completed lactations that included the diagnosis of the main health problems in the Langhill herd over the study period.

In addition to the health problems, factors evaluated for each cow prepartum (lactation before calving) and postpartum (lactation after calving) were: lactation number, genetic line, diet, live weight post-calving, condition score at calving, calving assistance, number of calves born, calf sex, total birth weight of calves, post-calving cow to calf weight ratio, live weight and condition score at drying off, length of drying off period, lactation length, calving interval and gestation length. The fertility measures evaluated were: days from calving to first service and calving to conception, days from calving to first heat observed, number of services, number of services per conception and conception success or failure. Feed intake, milk yield, milk composition, SCC, body condition score and live weight were split into four periods: one to 100 days in milk (DIM), 101 to 200 DIM and 201 to 300 DIM and for all DIM.

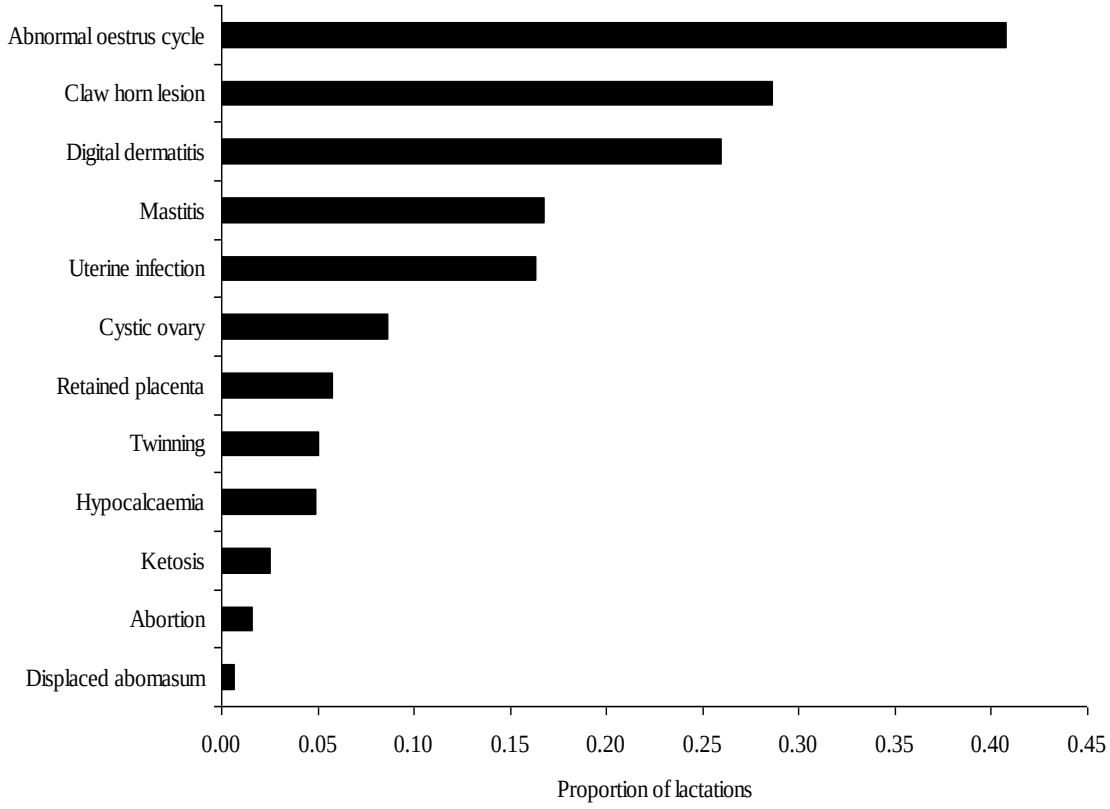

Fig. 17. Proportion of the 3,498 completed lactations that included the diagnosis of the main health problems in the Langhill herd over the study period from January 1990 to June 2008.

A.3.2 Statistical analysis

The data were analysed using Genstat Version 9.1 (Lawes Agricultural Trust, 2006). The effects of the explanatory variables (risk factors) on culling were investigated using a general linear mixed model. Cow identity was added to each model as a random effect. A binomial error distribution was assumed and a logistic link function was added. Wald tests, which use a χ^2 distribution, were used to examine the level of significance of the differences.

The continuous explanatory variables were separated into four classes using interquartile ranges of each variable, thus preventing outlying data from confounding the results. Each variable was analysed with culling (univariate analysis), to reduce the number of variables. The most significant variables from the univariate analysis were added first into a multivariate model. Variables that had confounding effects between each other were tested by running the model with and without each variable; any variable showing a significant effect was retained. Significance was attributed at $P < 0.05$.

A.4 Results

The culling rate for the Langhill herd from January 1990 to June 2008 was about 25% per year, with 59% occurring before the fourth lactation (494 of 838). Of the cows culled, 80% occurred at Farm 1 rather than at Farm 2 (674 of 838) and 68% of cows being culled (568 of 838) were classified as being involuntary. Of the cows classified as being involuntary culled, 58% occurred before their fourth lactation (330 of 568).

A.4.1 Risk factors for culling

Risk factors for culling are shown in Table 22. Culling was associated with cows that had an assisted calving ($P < 0.01$), aborted ($P < 0.01$) and/or suffered from mastitis ($P < 0.05$). Cows that were culled were also more likely to be older cows ($P < 0.01$), have a low number of milking days ($P < 0.001$) and/or a greater number of days from calving to

conception ($P < 0.01$). Culling was also highly associated with conception failure (r = 0.752, $P < 0.001$).

Table 22. Predicted means from the multivariate analyses showing the main risk factors associated with cows that were culled

Factor		Mean	Wald statistic	df	SED	*P value*
Farm	One	0.18	14.9	1	0.25	<0.001
	Two	0.06				
Calving assistance	No assistance	0.09	8.2	1	0.23	<0.01
	Assisted	0.14				
Aborted	No incidence	0.05	10.3	1	0.48	<0.01
	Incidence	0.20				
Mastitis	No incidence	0.09	5.3	1	0.22	<0.05
	Incidence	0.13				
Age at calving (months)	<27	0.07	13.5	3	0.26	<0.01
	27 to 40	0.08				
	41 to 60	0.13				
	>60	0.17				
Milking days (d)	<266	0.36	74.7	3	0.30	<0.001
	266 to 299	0.10				
	300 to 337	0.05				
	>337	0.06				
Calving to conception (d)	<74	0.06	14.2	3	0.29	<0.01
	74 to 97	0.10				
	98 to 135	0.11				
	>135	0.18				

SED = standard error of the difference between means.

A.5 Discussion and conclusions

The Langhill dairy herd is an experimental herd and is closely monitored and therefore the results of this study may not be representative of a commercial herd; the advantages of studying this dataset are that it is an extensive and detailed dataset on the same herd over a long period of time, with roughly equal numbers of cows in each genetic and feeding system group. Due to cows moving farms part way through the study period, 80% of the cows culled were at Farm 1. During the study period the average culling rate per year was 25% with 59% of cullings occurring before the fourth lactation. Veerkamp *et al.* (2001) reported a similar figure of 59% of cullings occurring before the fourth lactation in the national population. Bascom and Young (1998) concluded that the

optimum culling rate for farm profitability is between 25 to 30%, which the Langhill herd is within this range.

This study highlights the risk factors for culling and the high proportion of cows within the herd that could be classified as being involuntary culled. In this study 68% of cows culled were classified as involuntary, with 58% of cows classified as being involuntary culled being before their fourth lactation. The protocol for the research herd is to keep cows in the herd for at least three lactations unless cow welfare dictates that culling is necessary. The risk factors for culling associated with cows in the Langhill herd can be considered to be for voluntary or involuntary reasons. Risk factors that could be associated with cows that are involuntarily culled are an assisted calving, abortion, mastitis and a high number of days from calving to conception. In previous work the need for an assisted calving has been associated with the occurrence of twinning and/or uterine infection, which are both associated with culling (Bell and Roberts, 2007a and 2007b). As expected, older cows and cows with a fewer number of milking days are at risk of being culled, which could be for voluntary or involuntary reasons. By identifying the risk factors for the main reproductive problems that are seen in the herd (abnormal oestrus cycle, uterine infection, cystic ovary and abortion) the subsequent risk of a cow being culled due to an increased number of days from calving to conception and conception failure can be reduced. As also identified in this study, Bascom and Young (1998) put the main reasons for culling as reproduction, milk production and mastitis, which are all involuntary reasons for culling. By reducing the risks associated with poor reproductive and milking performance and the incidence of mastitis the number of cows culled for management reasons can be increased.

In conclusion, this study identified the specific risk factors for culling within the Langhill Holstein-Friesian dairy herd, which has been managed as an experimental herd for a number of years. This work could aid future breeding goals with regard to reducing the need for involuntary culling by indentifying the key factors associated with

the incidence of an assisted calving, abortion, mastitis and improving milking persistency and fertility performance within the Langhill herd.

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